APPENDIX A

TAXONOMIC CORRECTIONS AND EVALUATION

A.1. TAXONOMIC CORRECTIONS AND EVALUATIONS PERFORMED ON THE OHIO DATA SET

The Midwest Biodiversity Institute (MBI) developed a list of possible taxa that could affect the Invertebrate Condition Index (ICI) scoring via taxonomic refinement (splitting or lumping of taxa). MBI then conferred with senior Ohio Environmental Protection Agency (EPA) taxonomists (Mike Bolton and Jack Freda) to determine how to best address these changes. Their efforts primarily resulted in "combining of the" individual taxa designations of mayflies back into "*Baetis* sp." or "*Pseudocloeon* sp." as described in Table A-1. This process assured that changes found in the ICI calculated at reference sites for the historic and current periods would be reflecting biological responses to changing conditions and not changes in taxonomy. See results in Tables 6-7 and 6-8 of the main report for a summary of the impact of these taxonomic fixes on index values.

A.2. EVALUATION OF TAXA CORRECTIONS—NONMETRIC MULTIDIMENSIONAL SCALING (NMDS)

In the Maine, North Carolina, and Utah data sets, we used NMDS to evaluate whether the database 'fixes,' and in particular the taxonomic corrections and application of operational taxonomic unit (OTU) rules, were effective in minimizing changes over time due to taxonomic identification procedures rather than actual community changes. For the Ohio data set, taxonomic fixes were conducted by Ed Rankin and Chris Yoder of MBI and were straightforward, mainly recombining mayfly taxa for which refinements resulted in renaming or splitting of taxa since the historic time period during which reference communities were evaluated using the ICI. Postfacto NMDS evaluation was not deemed necessary for that application (see results in Tables 6-7 and 6-8 of the main report for a summary of the impact of these taxonomic fixes on index values). For the Maine, North Carolina, and Utah data sets, the NMDS ordinations were run before and after generating genus-level OTUs. Various grouping variables (i.e., year, month, collection method, taxonomy lab, ecoregion, watershed, etc.) were overlaid to look for trends. Figures A-1A through A-14B and Figures A-18 through A-22B show the NMDS plots that were generated as part of this exercise. Figures A-15 through A-17 show more details about number of identifications by species, genera, and families, as well as differences in total taxa identifications by laboratory. Table A-2 lists the laboratories references in Figure A-17.

Table A-1. Mayfly taxa from reference sites in Ohio that abruptly appeared (Later) or disappeared (Earlier) in the Ohio data set and explanation of change. Explanations were provided by Mike Bolton and Jack Freda of OH EPA

Taxa code	Taxon name	Appearance	Explanation of change
11010	*Acentrella* sp.	Later	Advancements in taxonomy allow this taxa to be distinguished from *Pseudocloeon* sp.
11014	*Acentrella turbida*	Later	Advancements in taxonomy allow this taxon to be distinguished from *Pseudocloeon* sp.
11015	*Acerpenna* sp.	Later	Advancements in taxonomy allow this taxon to be distinguished from Baetidae sp.
11018	*Acerpenna macdunnoughi*	Later	Advancements in taxonomy allow this taxon to be distinguished from Baetidae sp.
11020	*Acerpenna pygmaea*	Later	Advancements in taxonomy allow this taxon to be distinguished from Baetidae sp.
11110	*Acentrella parvula*	Later	Advancements in taxonomy allow this taxon to be distinguished from *Pseudocloeon* sp. or was renamed from *Pseudocloeon parvulum*
11115	*Baetis tricaudatus*	Later	Advancements in taxonomy allow this taxon to be distinguished from Baetidae sp.
11118	*Plauditus dubius*	Later	Advancements in taxonomy allow this taxon to be distinguished *Pseudocloeon* sp.
11119	*Plauditus dubius* or *P. virilis*	Later	Advancements in taxonomy allow this taxon to be distinguished *Pseudocloeon* sp.
11120	*Baetis flavistriga*	Later	Advancements in taxonomy allow this taxon to be distinguished from Baetidae sp.
11125	*Pseudocloeon frondale*	Later	Advancements in taxonomy allow this taxon to be distinguished from Baetidae sp.
11130	*Baetis intercalaris*	Later	Advancements in taxonomy allow this taxon to be distinguished from Baetidae sp.
11150	*Pseudocloeon propinquum*	Later	Advancements in taxonomy allow this taxon to be distinguished from Baetidae sp.
11155	*Plauditus punctiventris*	Later	Advancements in taxonomy allow this taxon to be distinguished *Pseudocloeon* sp.
11175	*Plauditus virilis*	Later	Advancements in taxonomy allow this taxon to be distinguished *Pseudocloeon* sp.

Table A-1. Mayfly taxa from reference sites in Ohio that abruptly appeared (Later) or disappeared (Earlier) in the Ohio data set and explanation of change. Explanations were provided by Mike Bolton and Jack Freda of OH EPA (continued)

| Taxa code	Taxon name	Appearance	Explanation of change
11250	*Centroptilum* sp. (w/o hindwing pads)	Later	Advancements in taxonomy allow this taxon to be distinguished *Cloeon* sp.
11400	*Centroptilum* sp. or *Procloeon* sp. (formerly in *Cloeon*	Earlier	Advancements in taxonomy allow this taxon to be distinguished *Cloeon* sp.
11430	*Diphetor hageni*	Later	Advancements in taxonomy allow this taxon to be distinguished from Baetidae sp.
11503	*Heterocloeon curiosum*	Later	Renamed *Heterocloeon* (H.) sp., *Heterocloeon* sp.
11600	*Paracloeodes* sp. 1	Later	Advancements in taxonomy allow this taxon to be distinguished from *Paracloeodes* sp.
11625	*Paracloeodes* sp. 3	Later	Advancements in taxonomy allow this taxon to be distinguished from *Paracloeodes* sp.
11645	*Procloeon* sp.	Later	Was earlier classified as *Centroptilum* sp. or *Cloeon* sp.
11650	*Procloeon* sp. (w/hindwing pads)	Later	Was earlier classified as *Cloeon* sp.
11651	*Procloeon* sp. (w/o hindwing pads)	Later	Was earlier classified as *Centroptilum* sp.
11670	*Procloeon irrubrum*	Later	Advancements in taxonomy allow this taxon to be distinguished from *Cloeon* sp.
11700	*Acentrella* sp. or *Plauditus* sp. (formerly in *Pseudoc*)	Earlier	Renamed as *Pseudocloeon* sp.
13010	*Leucrocuta hebe*	Earlier	Renamed as *Heptagenia hebe*
13030	*Leucrocuta maculipennis*	Earlier	Renamed as *Heptagenia maculipennis*
14501	Leptophlebiidae	Earlier	Now coded as *Leptophlebia* sp.
14900	*Leptophlebia* sp.	Later	*Leptophlebia* sp.
14950	*Leptophlebia* sp. or *Paraleptophlebia* sp.	Later	Small specimens lumped
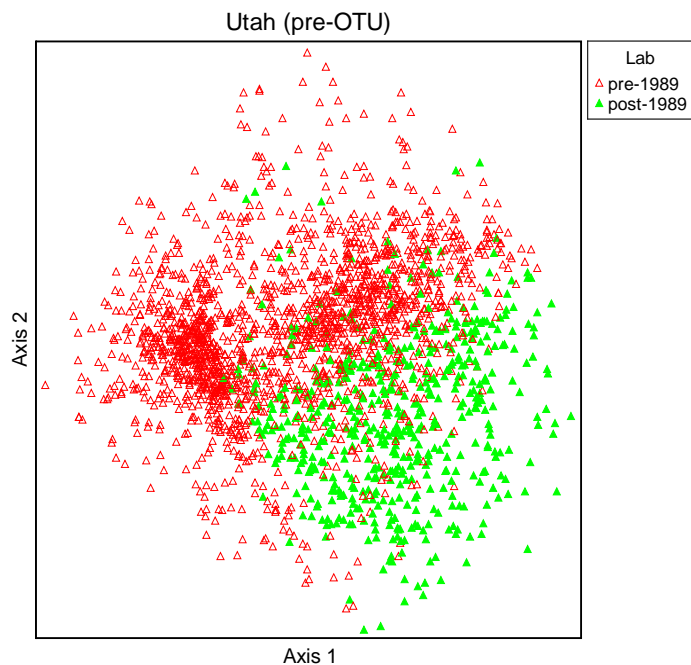
Figure A-1A. Pre-OTU (genus) NMDS plot when lab is used as the grouping variable.
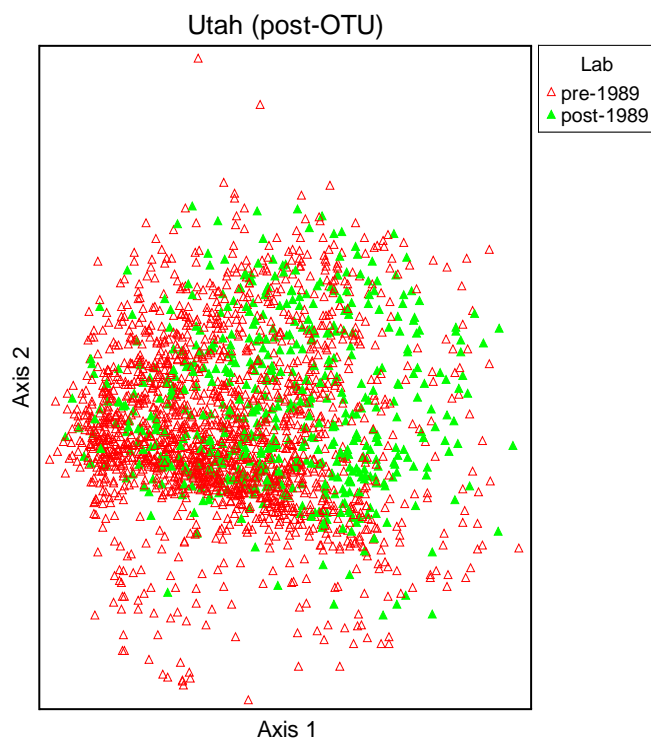

Figure A-1B. Post-OTU (genus) NMDS plot when lab is used as the grouping variable.
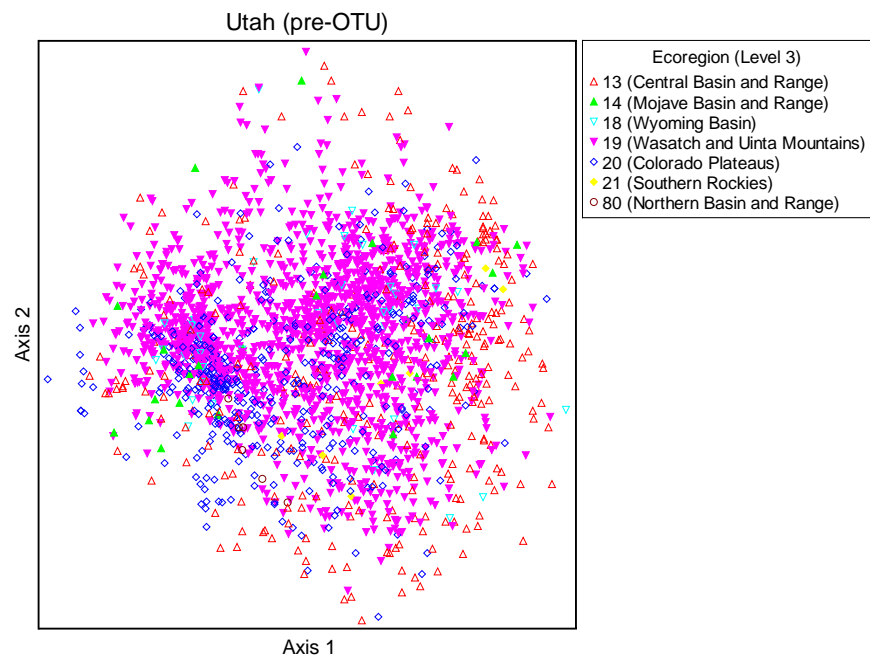
Figure A-2A. Pre-OTU (genus) NMDS plot when Level 3 ecoregion is used as the grouping variable.
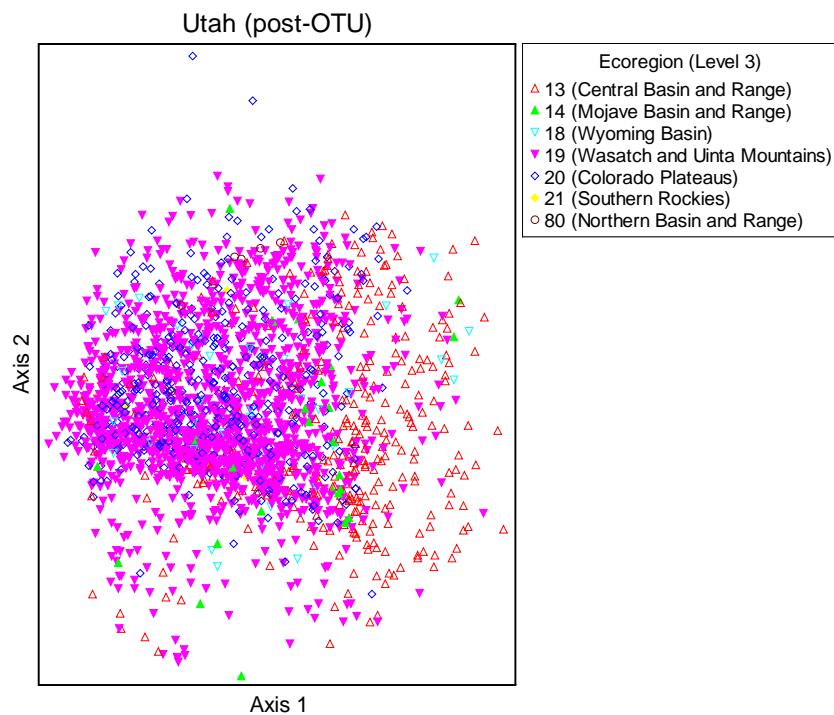

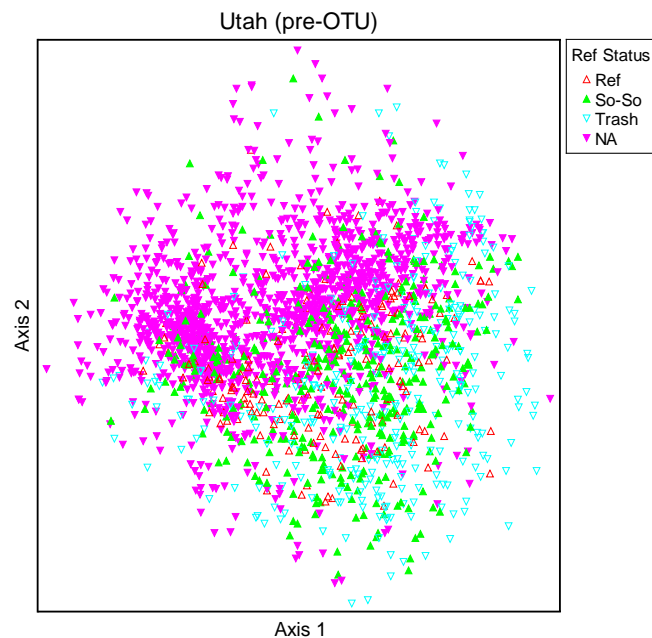**Figure A-2B. Post-OTU (genus) NMDS plot when Level 3 ecoregion is used as the grouping variable.**

Figure A-3A. Pre-OTU (genus) NMDS plot when reference status is used as the grouping variable.
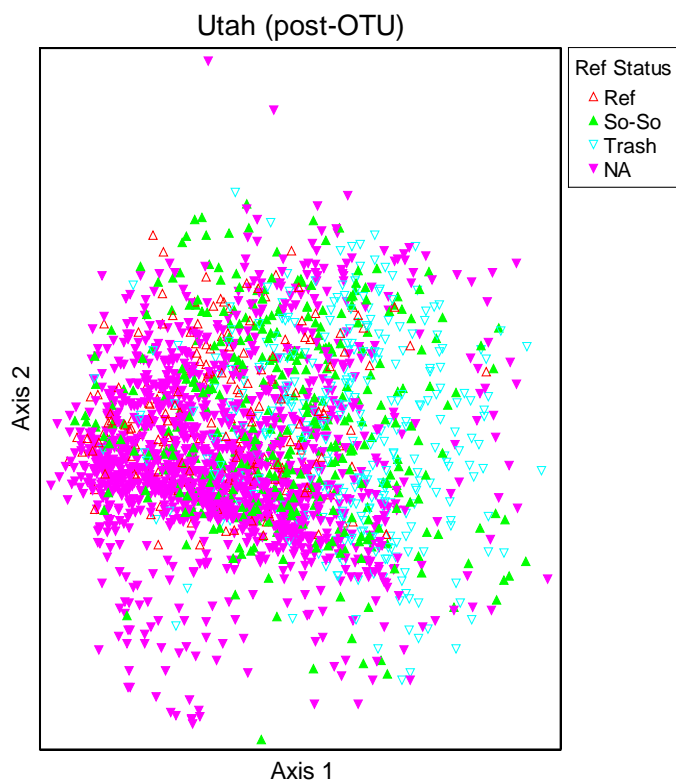

Figure A-3B. Post-OTU (genus) NMDS plot when reference status is used as the grouping variable.
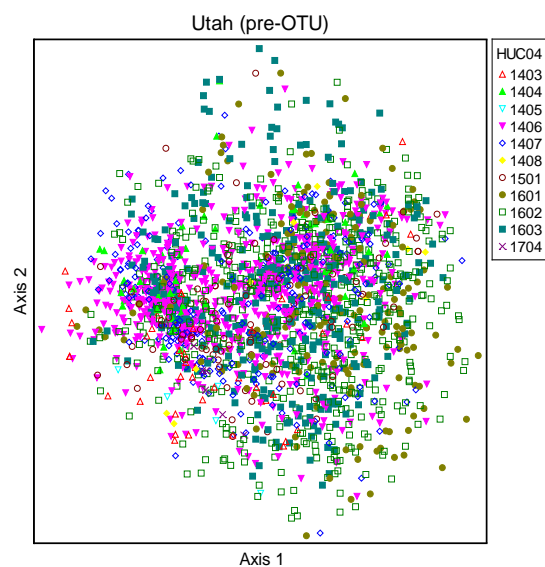
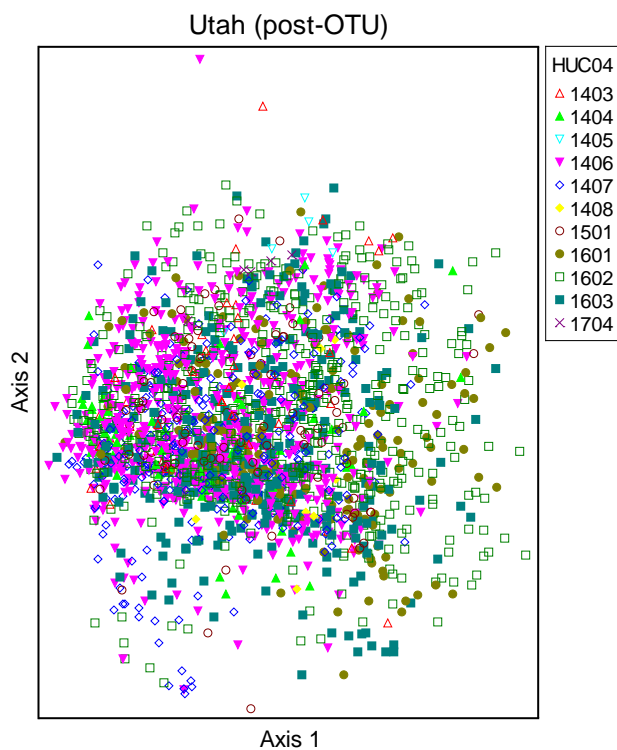**Figure A-4A. Pre-OTU (genus) NMDS plot when Hydrologic Unit Code (HUC)-04 is used as the grouping variable.**

Figure A-4B. Post-OTU (genus) NMDS plot when HUC-04 is used as the grouping variable.

A-8

Figure A-5A. Pre-OTU (genus) NMDS plot when reference status is used as the grouping variable. Trends related to latitude are also evaluated.

Figure A-5B. Post-OTU (genus) NMDS plot when reference status is used as the grouping variable. Trends related to latitude are also evaluated.
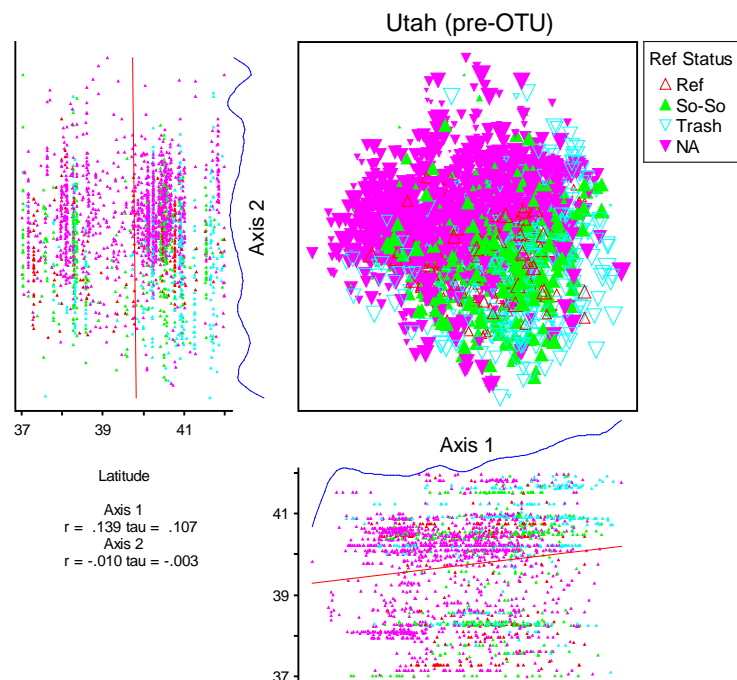
Figure A-6A. Pre-OTU (genus) NMDS plot when reference status is used as the grouping variable. Trends related to longitude are also evaluated.
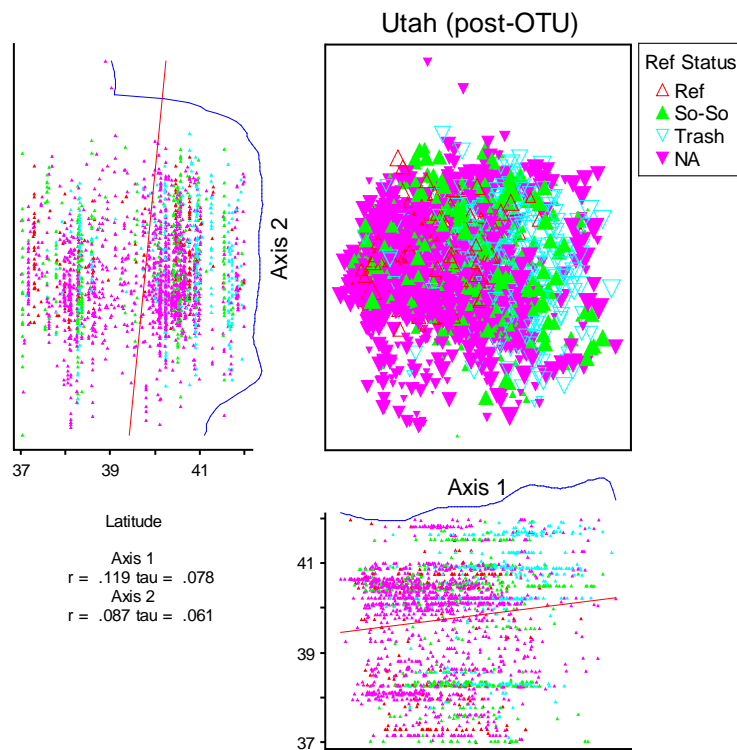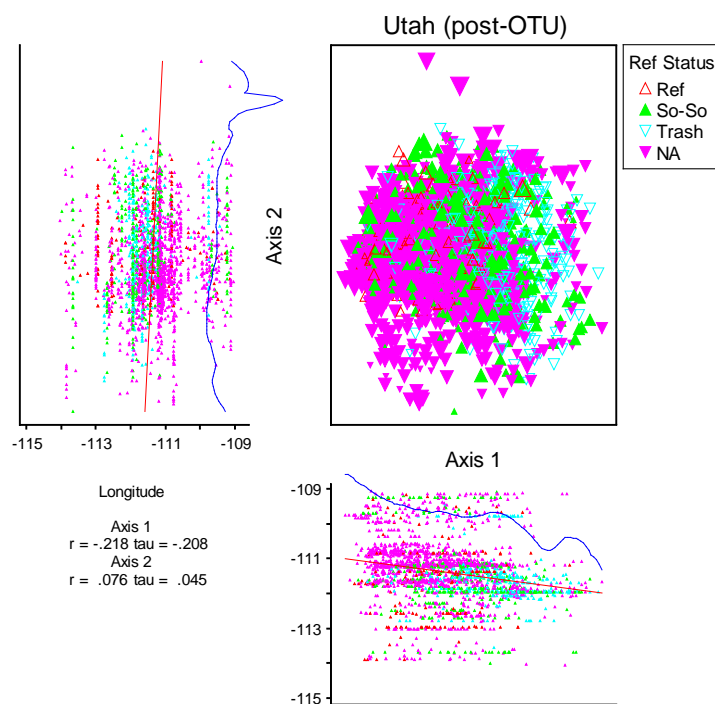

Figure A-6B. Post-OTU (genus) NMDS plot when reference status is used as the grouping variable. Trends related to longitude are also evaluated.
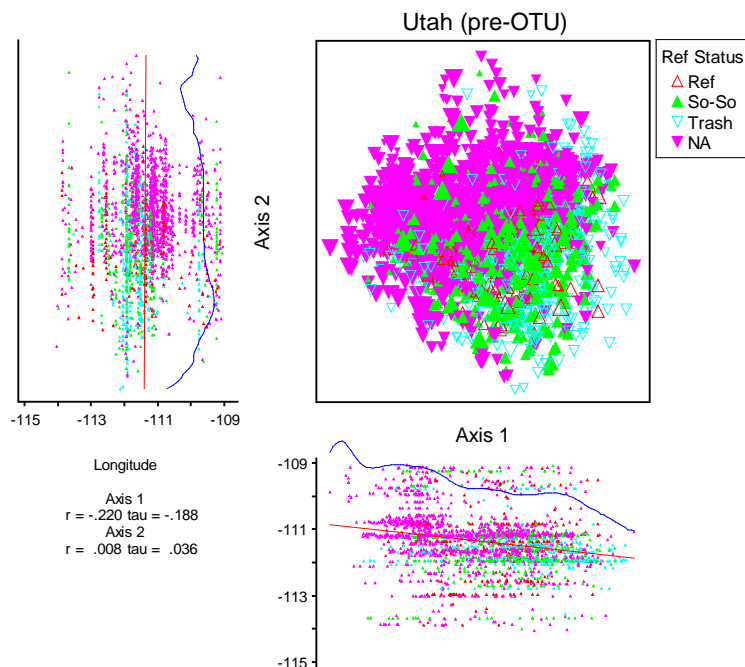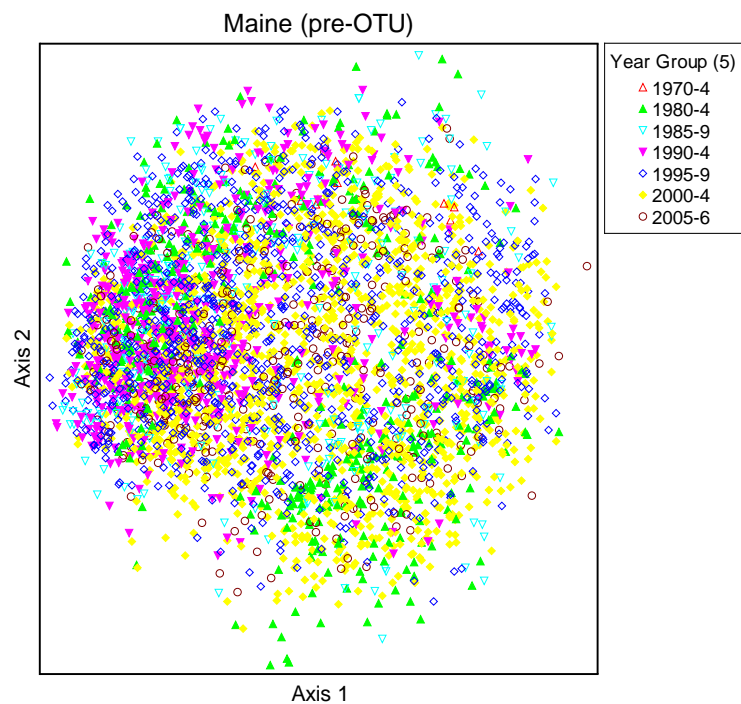
Figure A-7A. Pre-OTU (genus) NMDS plot using sample years (5-year increments) as the grouping variable.
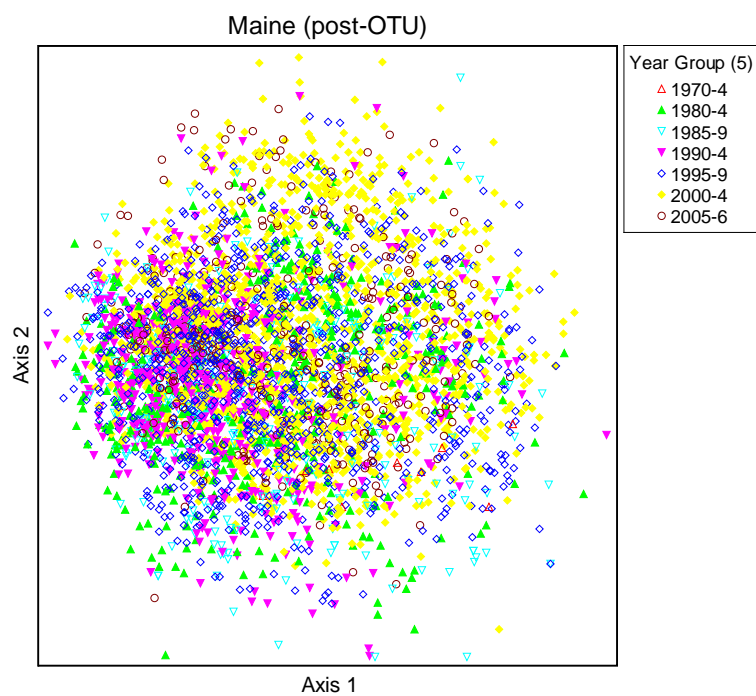
Figure A-7B. Post-OTU (genus) NMDS plot using sample years (5-year increments) as the grouping variable.
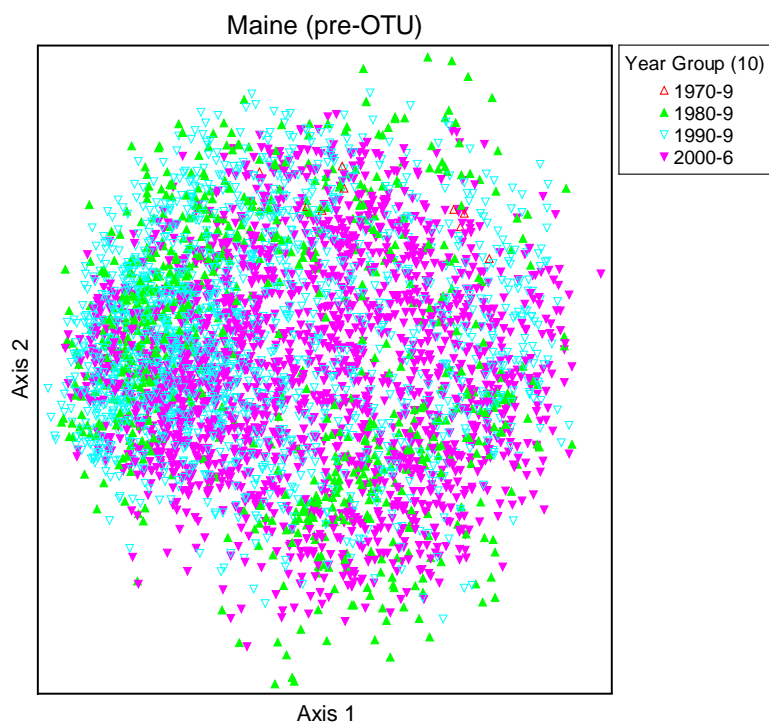
Figure A-8A. Pre-OTU (genus) NMDS plot using sample years (10-year increments) as the grouping variable.
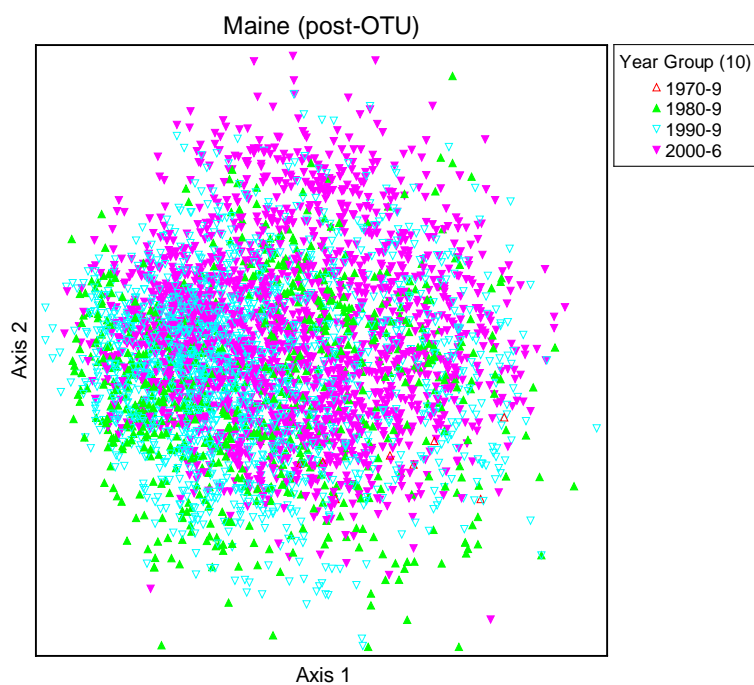
Figure A-8B. Post-OTU (genus) NMDS plot using sample years (10-year increments) as the grouping variable.
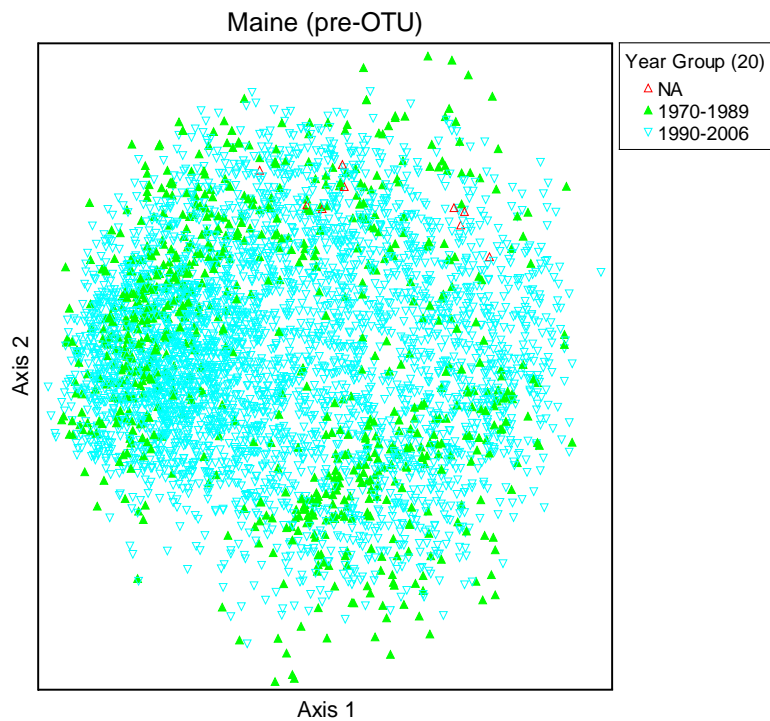
Figure A-9A. Pre-OTU (genus) NMDS plot using sample years (20-year increments) as the grouping variable.
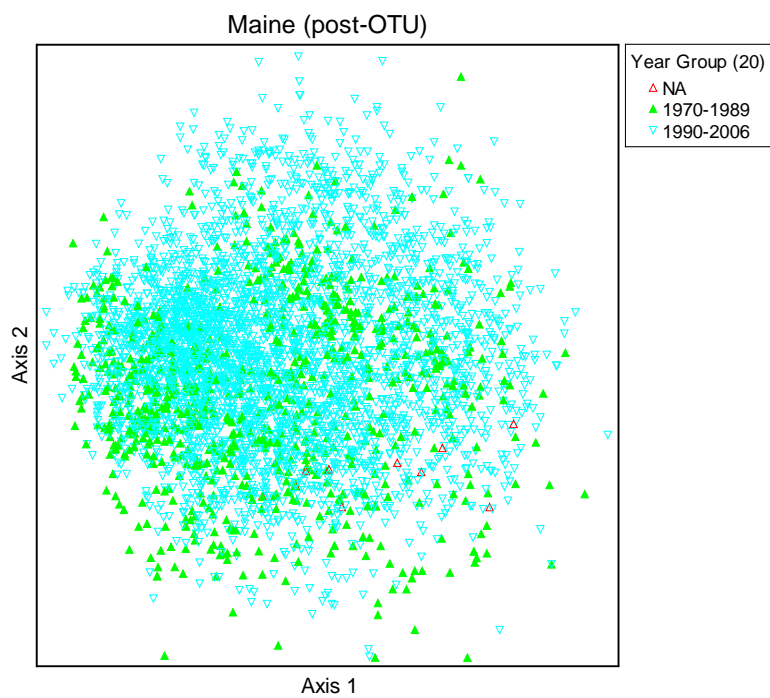
Figure A-9B. Post-OTU (genus) NMDS plot using sample years (20-year increments) as the grouping variable.
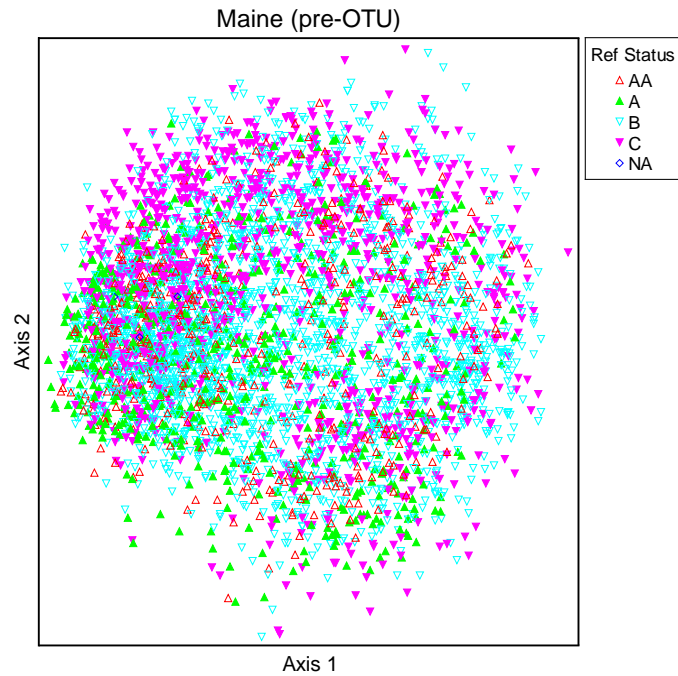
Figure A-10A. Pre-OTU (genus) NMDS plot when reference status is used as the grouping variable.
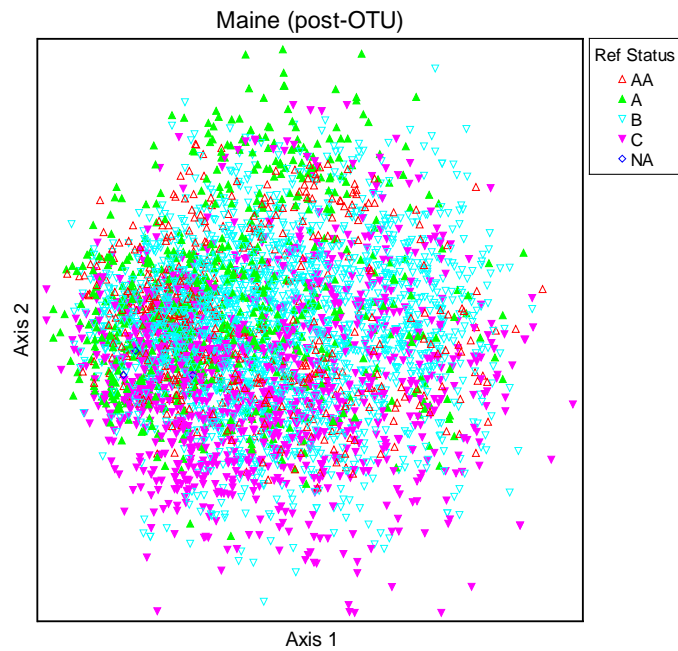
Figure A-10B. Post-OTU (genus) NMDS plot when reference status is used as the grouping variable.
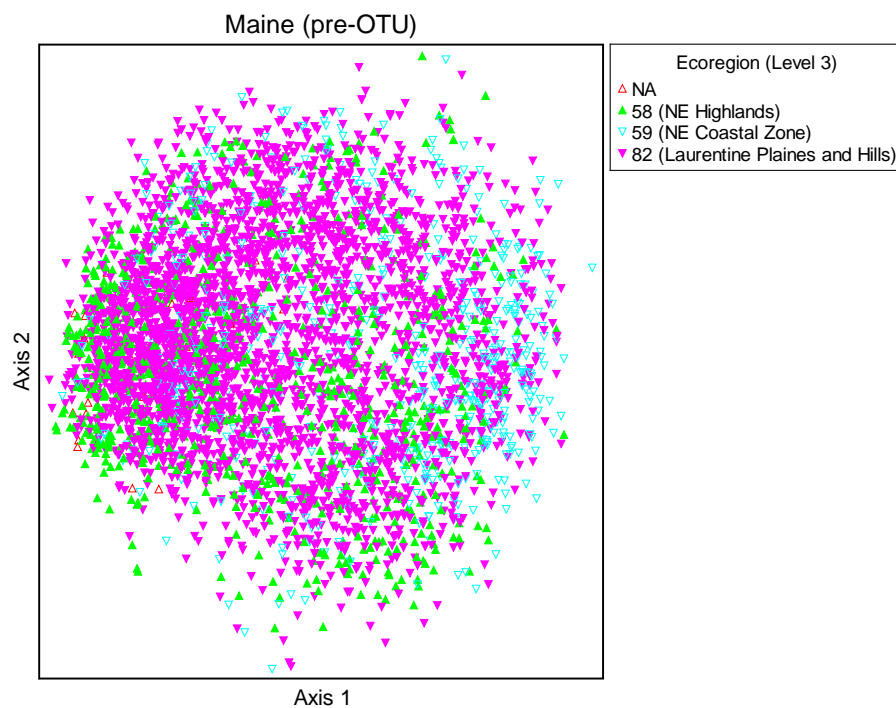
Figure A-11A. Pre-OTU (genus) NMDS plot when Level 3 ecoregion is used as the grouping variable.
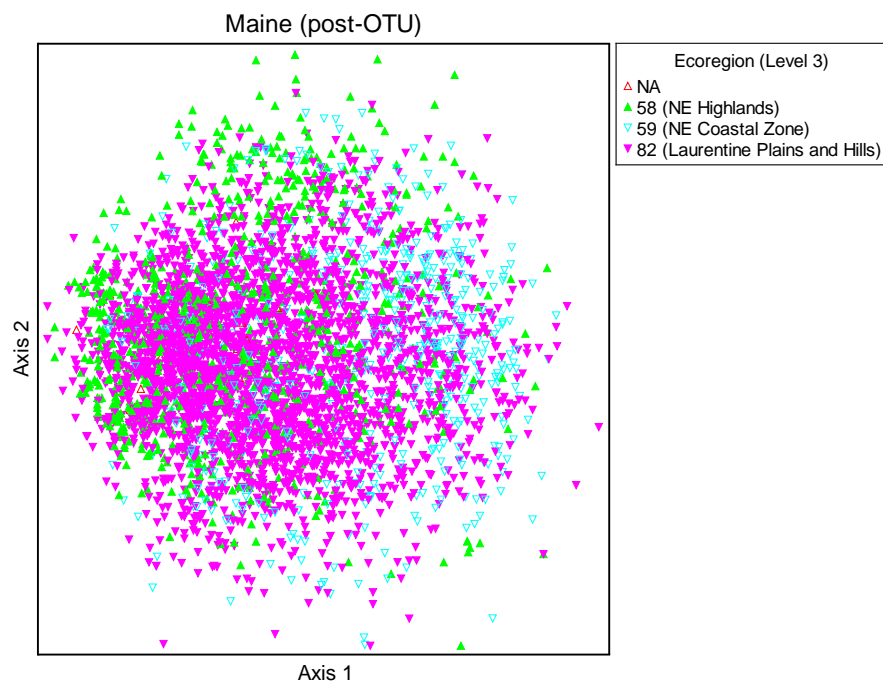
Figure A-11B. Post-OTU (genus) NMDS plot when Level 3 ecoregion is used as the grouping variable.
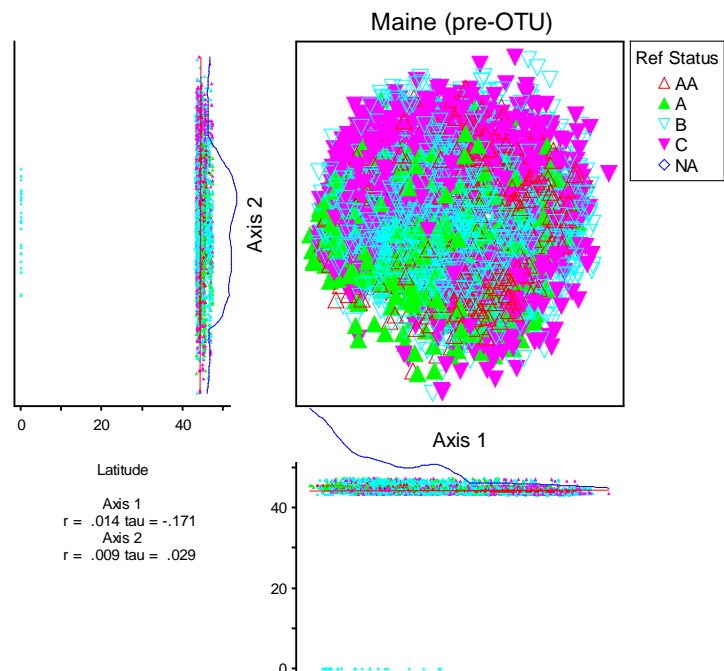
Figure A-12A. Pre-OTU (genus) NMDS plot when reference status is used as the grouping variable. Trends related to latitude are also evaluated.
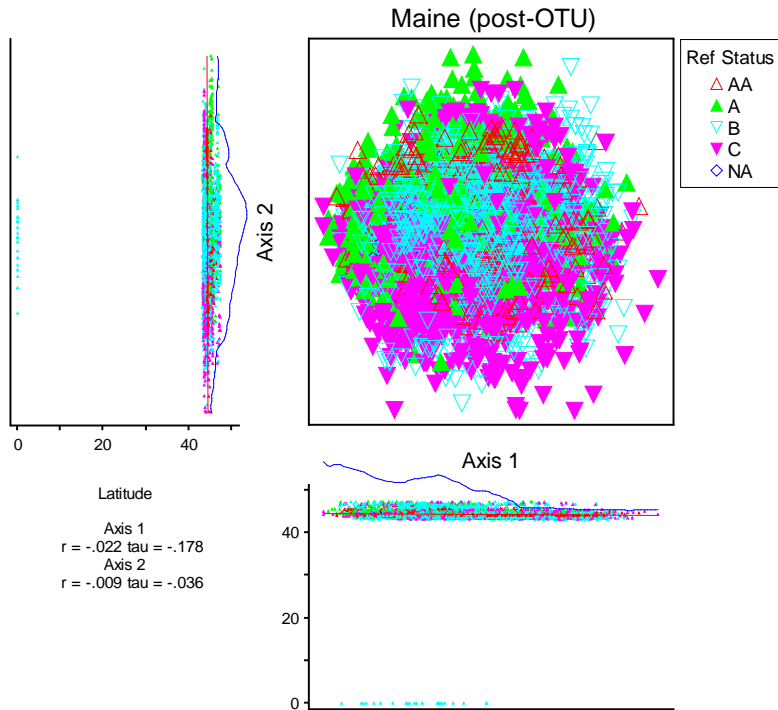
Figure A-12B. Post-OTU (genus) NMDS plot when reference status is used as the grouping variable. Trends related to latitude are also evaluated.
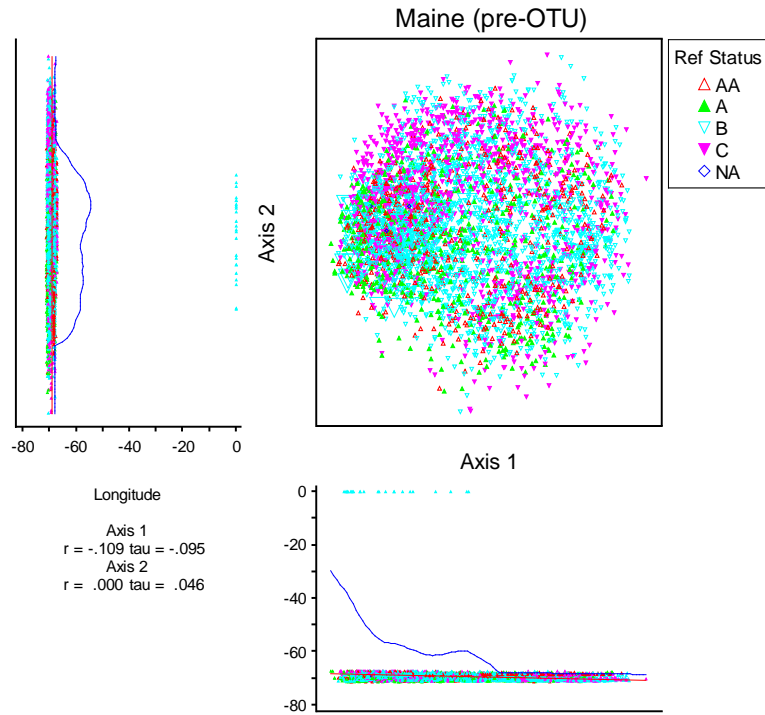
Figure A-13A. Pre-OTU (genus) NMDS plot when reference status is used as the grouping variable. Trends related to longitude are also evaluated.
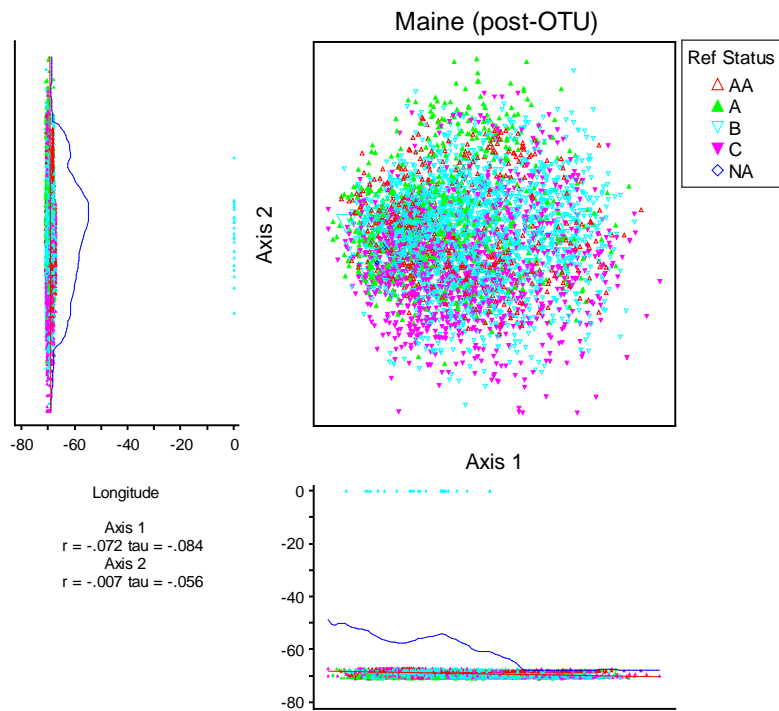
Figure A-13B. Post-OTU (genus) NMDS plot when reference status is used as the grouping variable. Trends related to longitude are also evaluated.
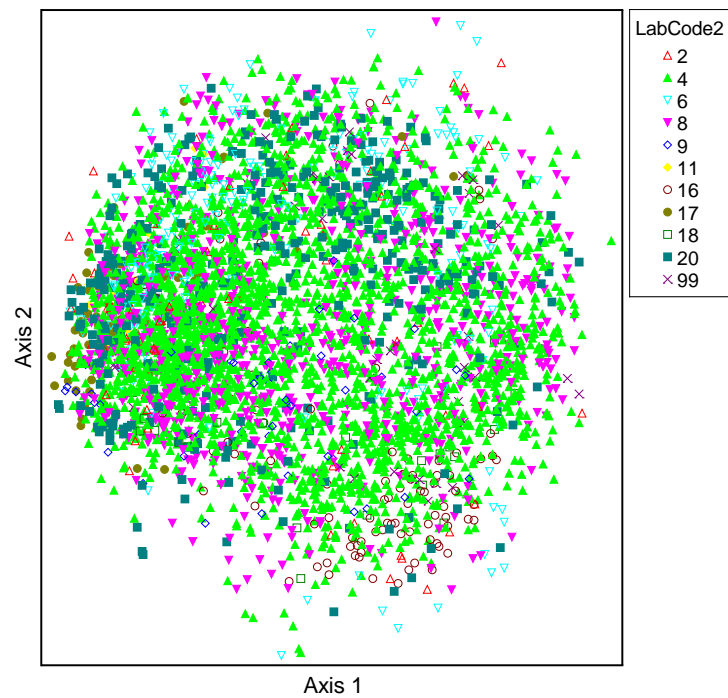
Figure A-14A. Pre-OTU (genus) NMDS plot for Maine data when lab is used as the grouping variable.
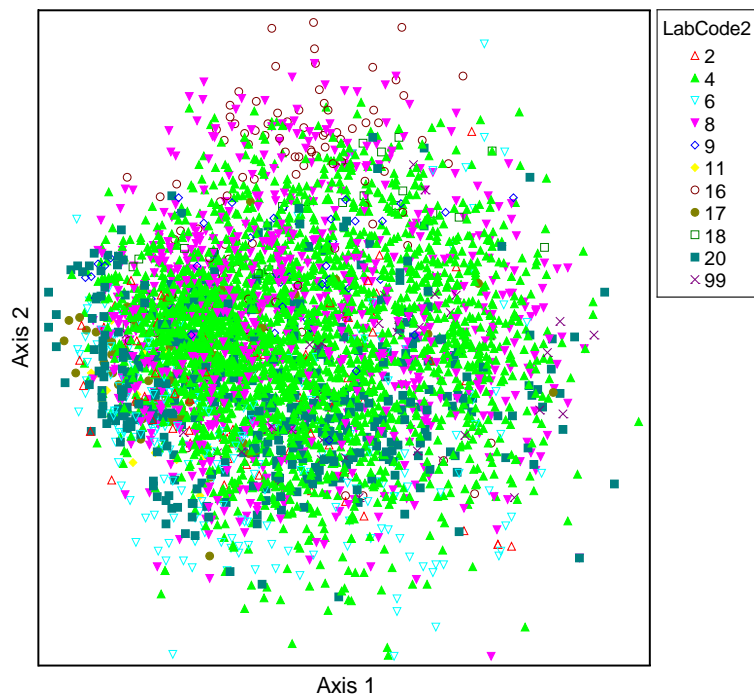
Figure A-14B. Post-OTU (genus) NMDS plot for Maine data when lab is used as the grouping variable.
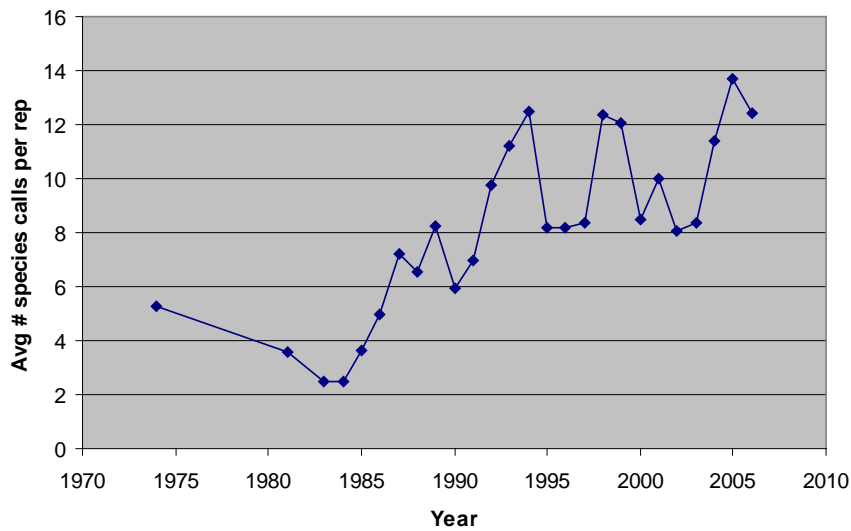
Figure A-15A. Average number of species-level identifications per replicate sample per year in the Maine database (using original data; not adjusted for OTUs).
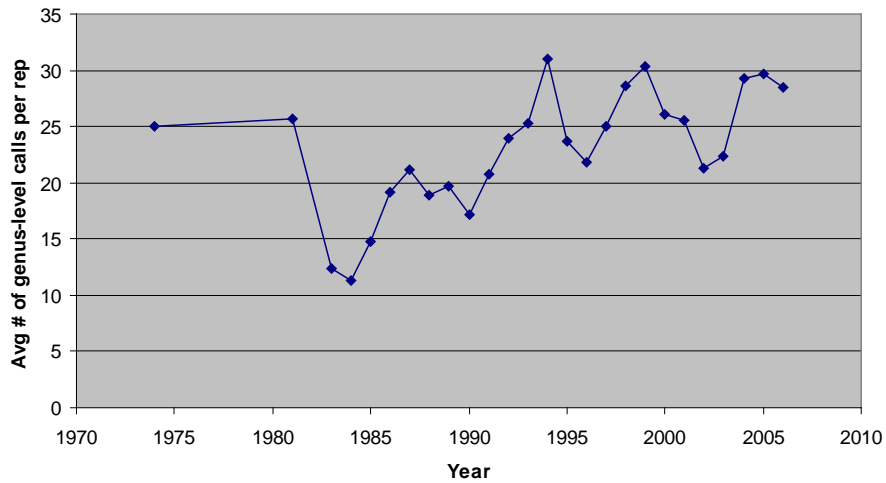
Figure A-15B. Average number of genus-level identifications per replicate sample per year in the Maine database (using original data; not adjusted for OTUs).
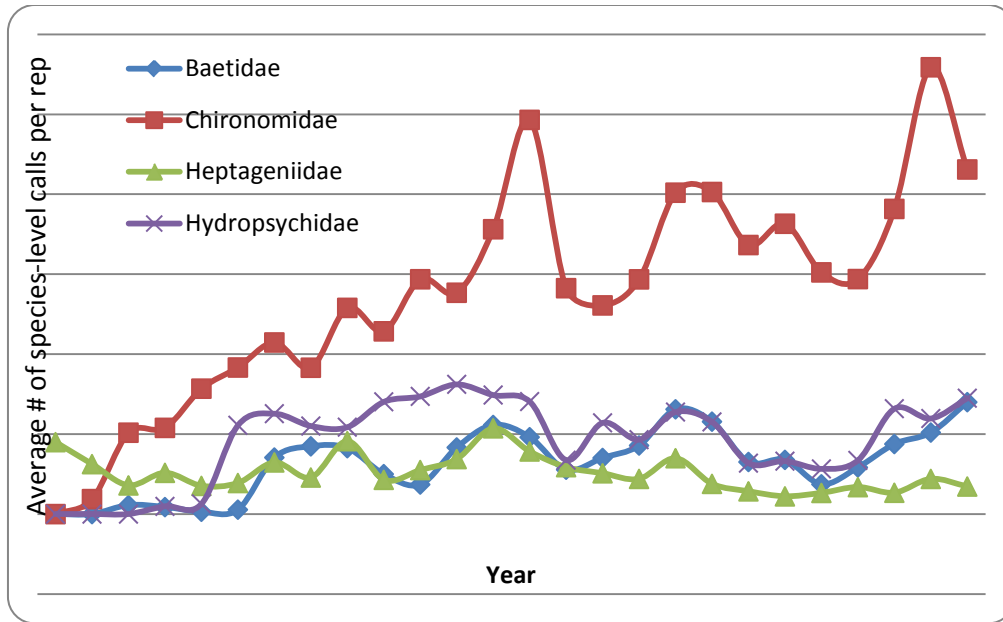
Figure A-16A. Average number of species-level identifications per replicate sample per year for selected families in the Maine database (using original data; not adjusted for OTUs).
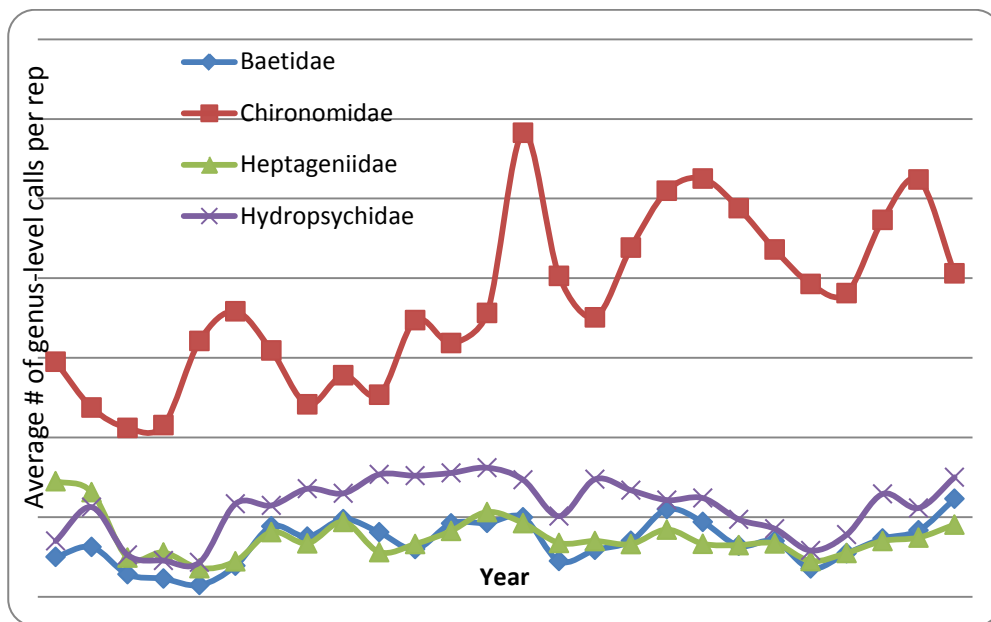
Figure A-16B. Average number of genus-level identifications per replicate sample per year for selected families in the Maine database (using original data; not adjusted for OTUs).
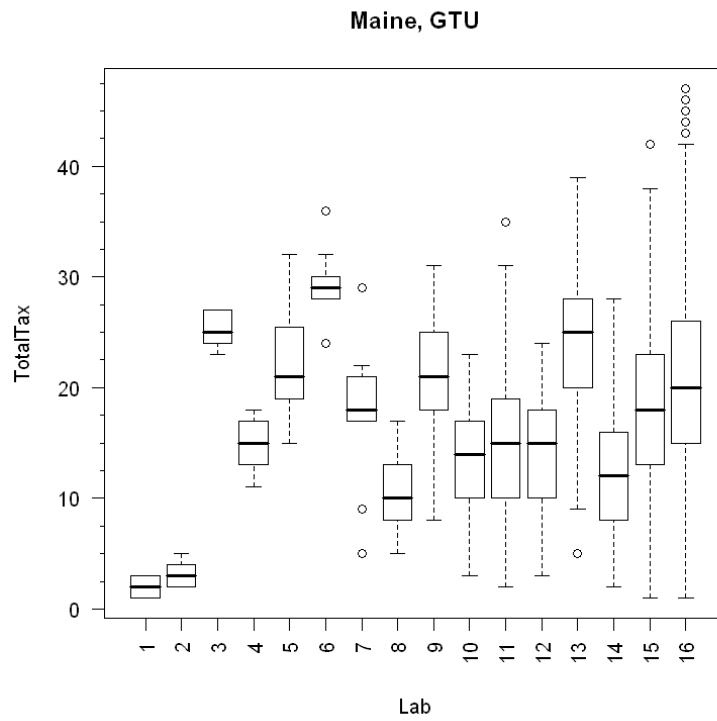
Figure A-17. Distribution of the total number of taxa (average per replicate) among laboratories in Maine.

Table A-2. List of 16 different individuals or labs that performed taxonomic analyses on Maine benthic samples during the study period 1983−2006. Per communication with Leon Tsomides Maine Department of Environmental Protection (ME DEP), some adjustments were made to taxonomy produced from different sources to assure consistency

Lab	Year_min	Year_max	#Samp	LabNum
BILLIE BESSIE	1996	1996	2	1
DAVID COURTEMANCH	1983	1983	5	2
B.A.R ENVIRONM	1994	1994	6	3
WOODWARD CLYDE	1981	1981	6	4
Unknown	1995	1995	7	5
BBL SCIENCES	2004	2004	9	6
CF RABENI	1974	1974	10	7
QST ENVIRONMENTAL (BOWATER)	1994	1996	20	8
CHRIS PINNUTO	2000	2000	22	9
NORMANDEAU	1989	1999	45	10
SUSAN DAVIES	1981	1989	74	11
NEW BRUNSWICK	1999	2001	84	12
IDAHO ECOANALYSTS	1999	2005	100	13
TERRY MINGO	1983	1987	254	14
LOTIC	1988	2006	743	15
MICHAEL WINNELL	1983	2006	2,509	16
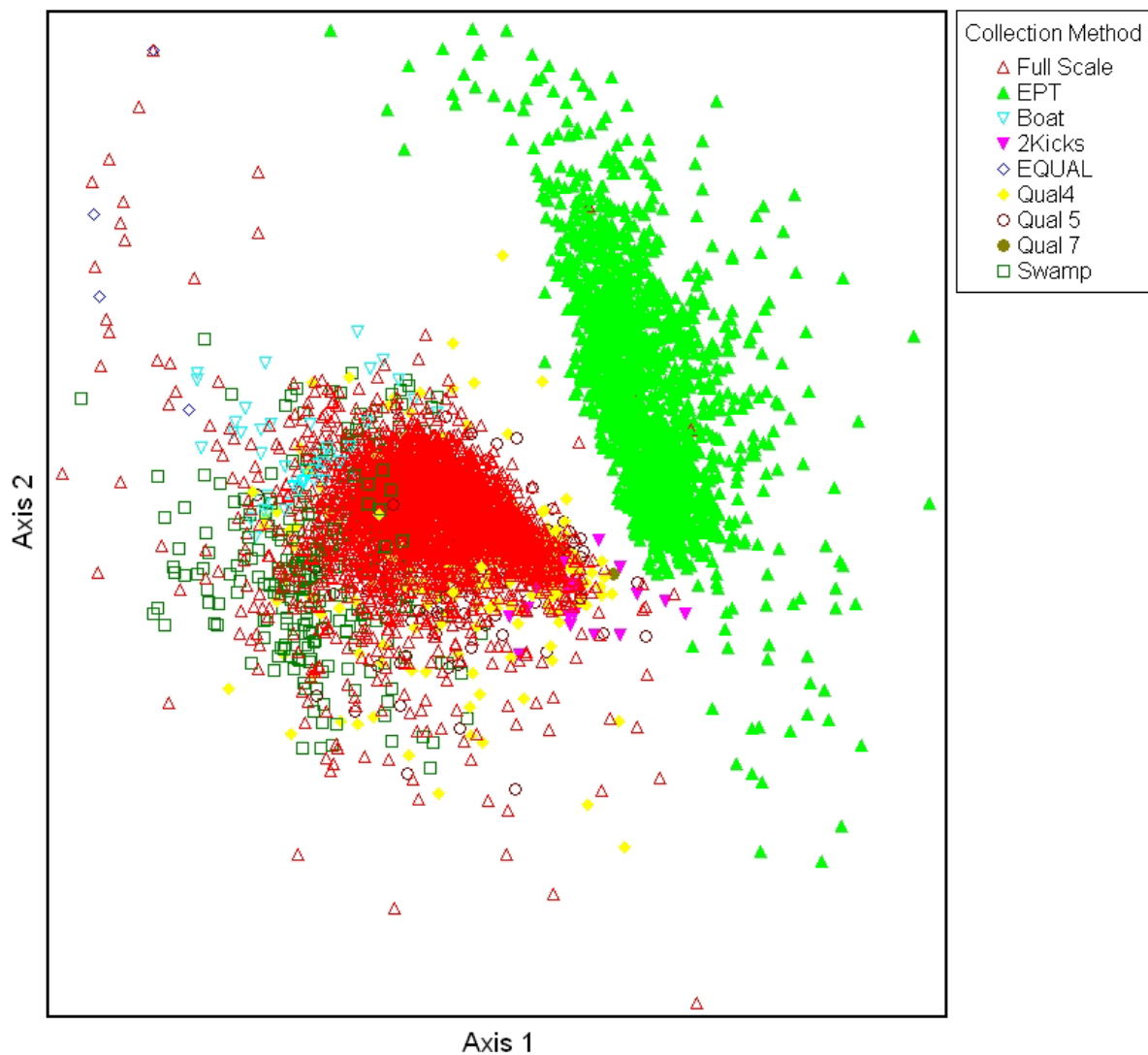
Figure A-18. Preliminary North Carolina NMDS plot (genus-level OTU) using collection method as the grouping variable.
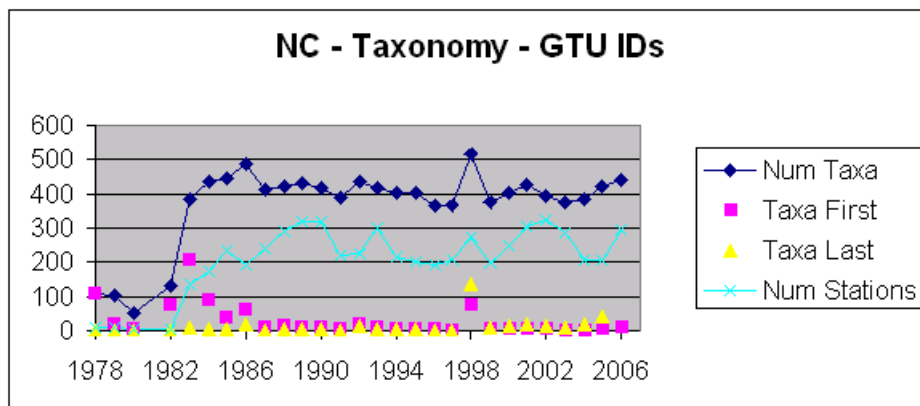
Figure A-19A. North Carolina genus-level OTU (GTU) data using all collection methods. "Num Taxa" refers to the total number of taxa recorded in a particular year; "Taxa First" refers to the number of taxa that appear in the database for the first time in a particular year; "Taxa Last" refers to the number of taxa that appear in the database for the last time in a particular year; "Num Stations" refers to the number of stations sampled in a particular year.
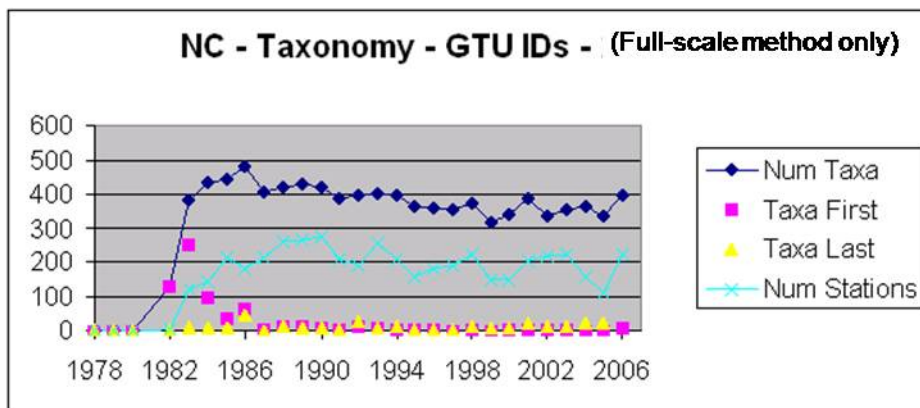
Figure A-19B. North Carolina GTU using data from only the Full-scale collection method. "Num Taxa" refers to the total number of taxa recorded in a particular year; "Taxa First" refers to the number of taxa that appear in the database for the first time in a particular year; "Taxa Last" refers to the number of taxa that appear in the database for the last time in a particular year; "Num Stations" refers to the number of stations sampled in a particular year.
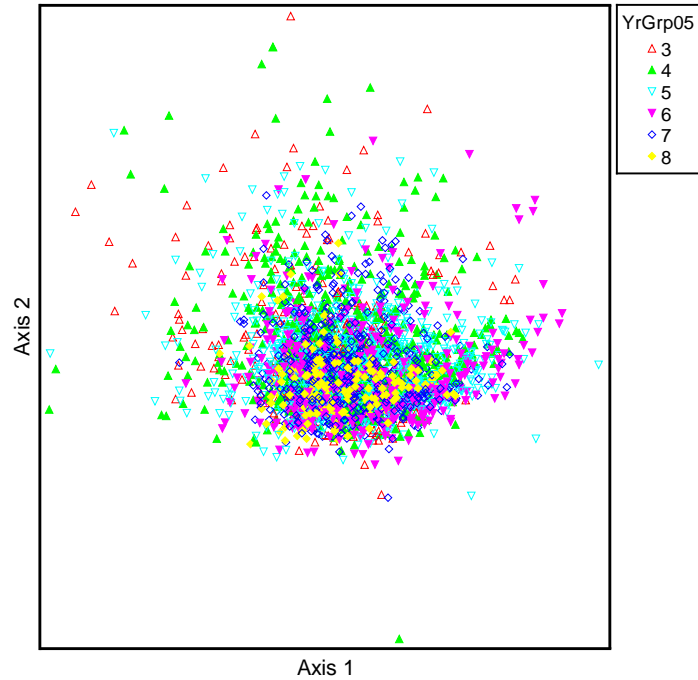
Figure A-20A. Pre-OTU (genus) NMDS plot for North Carolina data when year (5-year increments) is used as the grouping variable, and only full-scale collection method data are used.
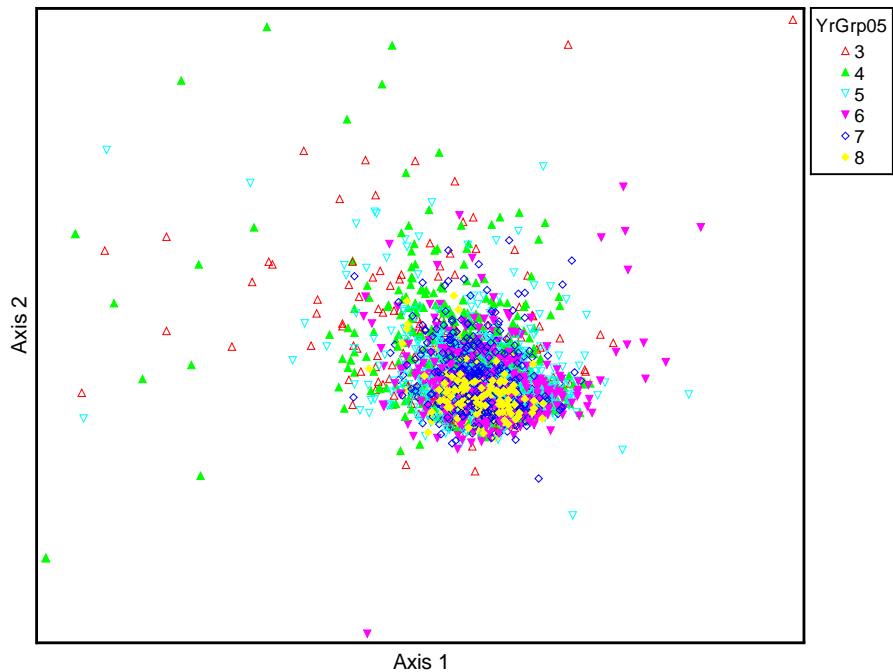
Figure A-20B. Post-OTU (genus) NMDS plot for North Carolina data when year (5-year increments) is used as the grouping variable, and only full-scale collection method data are used.
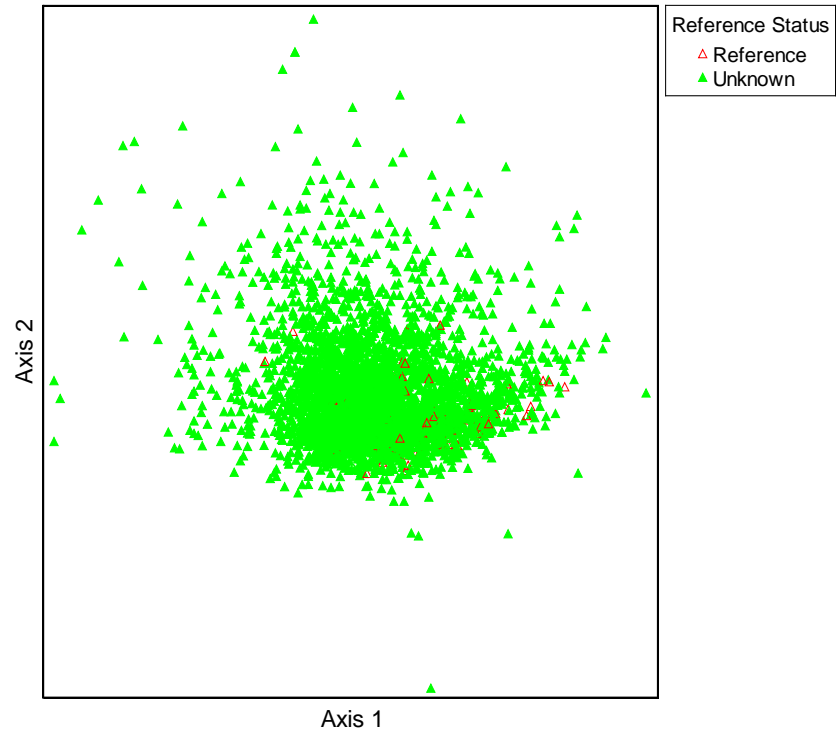
Figure A-21A. Pre-OTU (genus) NMDS plot for North Carolina data using reference status as the grouping variable, and only full-scale collection method data are used.
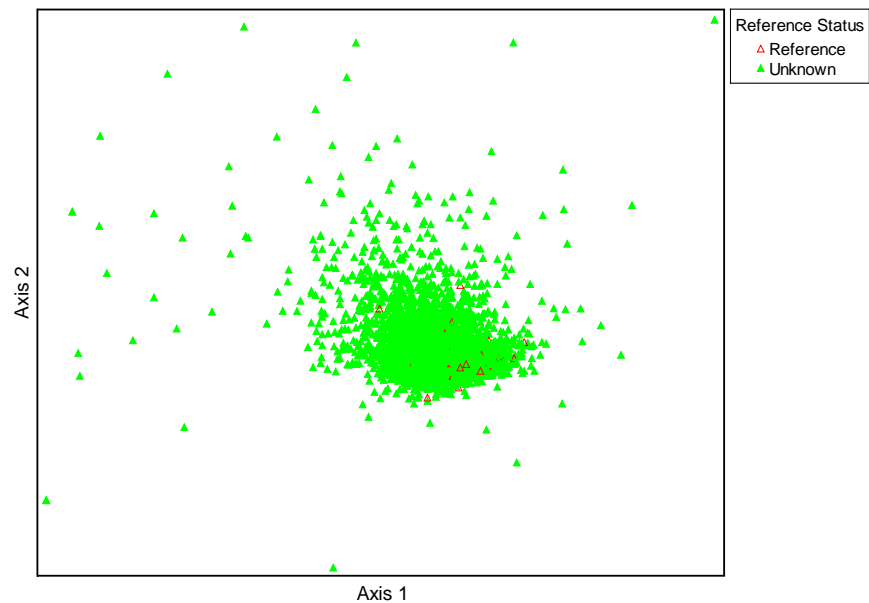
Figure A-21B. Post-OTU (genus) NMDS plot for North Carolina data using reference status as the grouping variable, and only full-scale collection method data are used.
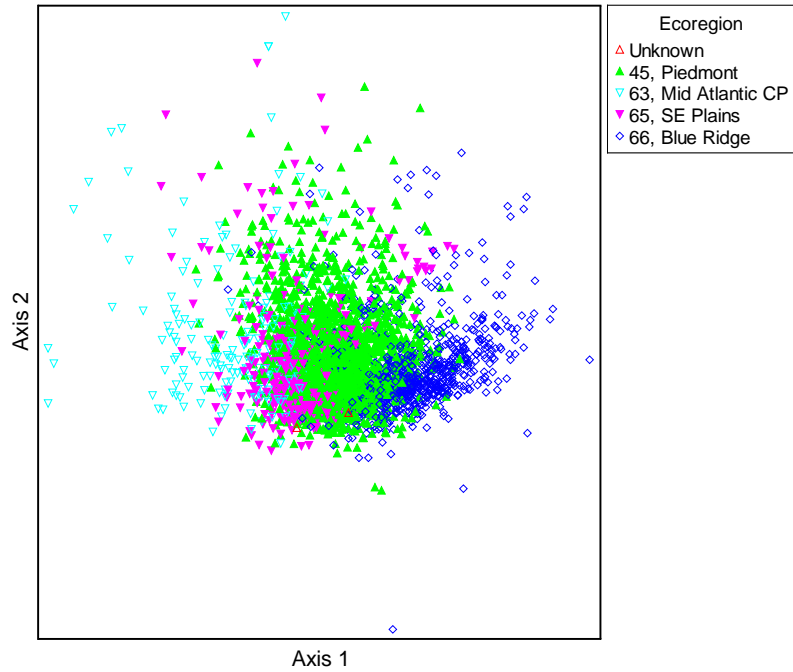
Figure A-22A. Pre-OTU (genus) NMDS plot for North Carolina data using Level 3 ecoregion as the grouping variable, and only full-scale collection method data are used.
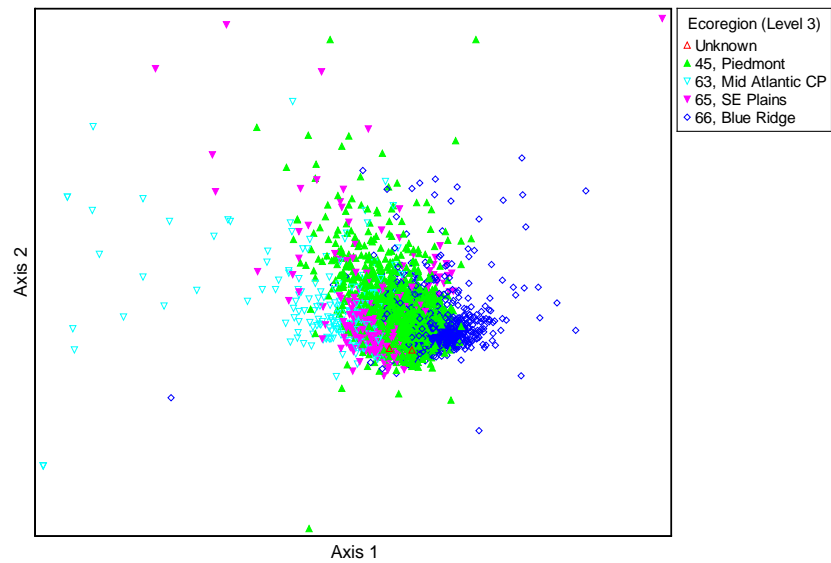
Figure A-22B. Post-OTU (genus) NMDS plot for North Carolina data using Level 3 ecoregion as the grouping variable, and only full-scale collection method data are used.

APPENDIX B

ADDITIONAL ANALYSES PERFORMED ON UTAH DATA

B.1. HYDROLOGIC ANALYSIS PERFORMED ON THE UTAH DATA SET

Figure B-1 shows the locations of the 43 Utah biological sampling stations that we associated with United States Geological Service (USGS) stream gages.
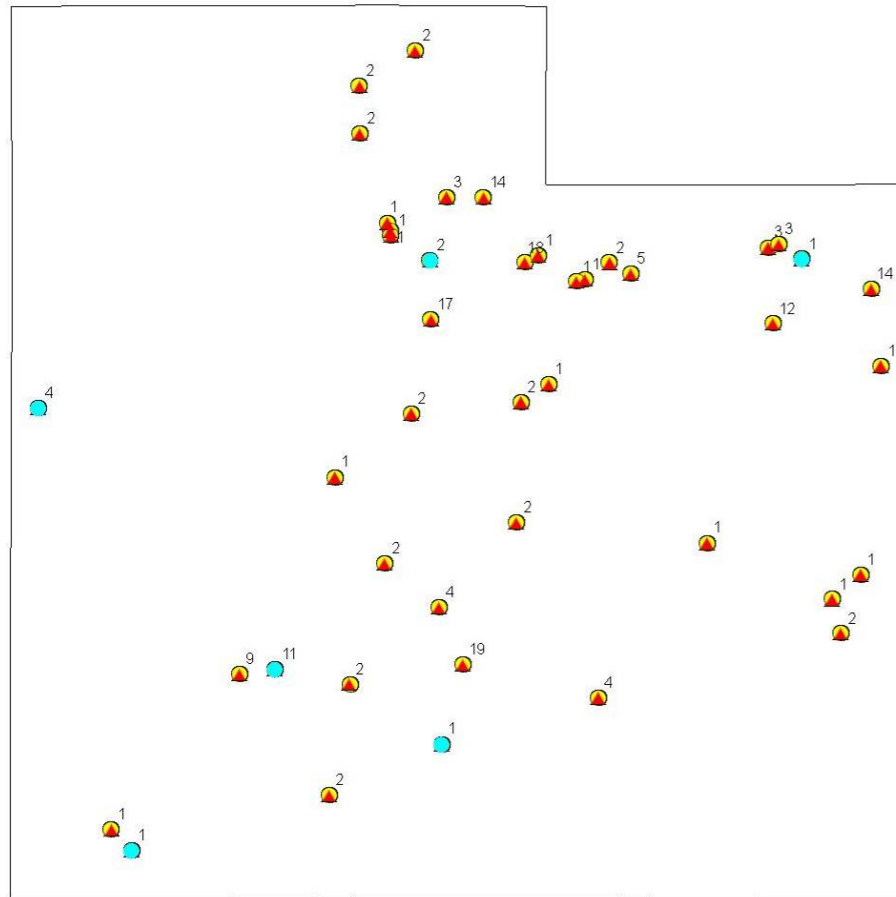
Figure B-1. Locations of the 43 Utah biological sampling stations (red triangles) and associated USGS stream gages (yellow circles). Stations that are highlighted in blue are classified as reference sites by Utah DEQ Division of Water Quality. The numbers next to the sites are the number of years of data that were available for each station.

Table B-1 shows results from the weighted-average modeling for the 3-day annual minima indicators of hydrologic alteration (IHA) parameters.

Table B-1. Weighted-average indicator values for annual minima, 3-day means

3-Day annual minima					
Taxa	Optimum	Tolerance	Rank_opt	Rank_tol	Count
Pisidium	0.030	0.04	1	2	16
Ambrysus	0.041	0.05	1	3	17
Mayatrichia/*Neotrichia*	0.045	0.03	1	2	16
Neotrichia	0.046	0.04	1	2	12
Leuctridae	0.049	0.03	1	1	24
Asellidae	0.050	0.06	1	4	45
Lymnaea	0.056	0.04	1	3	15
Zapada	0.057	0.04	1	3	35
Neothremma	0.059	0.04	1	3	19
Physella	0.060	0.06	2	5	13
Skwala	0.061	0.02	2	1	31
Petrophila	0.062	0.05	2	4	36
Coenagrionidae	0.064	0.07	2	6	36
Bibiocephala	0.065	0.01	2	1	17
Cultus	0.066	0.04	2	3	20
Serratella	0.067	0.04	2	2	11
Dytiscidae	0.068	0.04	2	2	10
Pelecypoda	0.069	0.06	2	5	44
Hesperoperla	0.069	0.05	2	4	33
Epeorus	0.070	0.04	2	2	92
Physa	0.071	0.06	2	5	54
Claassenia	0.072	0.03	3	1	12
Podmosta	0.072	0.03	3	1	10
Tipula	0.072	0.05	3	4	31
Capniidae	0.073	0.05	3	4	38
Apatania	0.073	0.02	3	1	20
Oecetis	0.073	0.04	3	2	45

Table B-1. Weighted-average indicator values for annual minima, 3-day means (continued)

Taxa	Optimum	Tolerance	Rank_opt	Rank_tol	Count
3-Day annual minima					
Baetidae	0.073	0.06	3	6	277
Heptagenia	0.075	0.05	3	4	58
Pteronarcella	0.076	0.04	3	2	91
Ephemerella	0.076	0.05	3	4	149
Chloroperlidae	0.076	0.04	3	2	105
Hemerodromia	0.076	0.07	3	6	103
Antocha	0.077	0.05	4	3	126
Ostracoda	0.077	0.06	4	5	96
Lepidostoma	0.077	0.05	4	4	88
Paraleptophlebia	0.078	0.04	4	2	96
Arctopsyche	0.078	0.05	4	3	99
Rhithrogena	0.078	0.04	4	3	127
Simuliidae	0.079	0.06	4	5	234
Chelifera	0.079	0.06	4	5	98
Isoperla	0.080	0.04	4	3	105
Cheumatopsyche	0.080	0.07	4	6	55
Rhyacophilidae	0.080	0.05	4	4	98
Cinygmula	0.080	0.05	4	3	90
Optioservus	0.080	0.06	4	5	148
Glossosoma	0.081	0.05	4	4	60
Acarina	0.081	0.06	4	5	268
Zaitzevia	0.081	0.05	4	4	97
Planaria	0.082	0.07	4	7	90
Leptohyphidae	0.082	0.07	5	6	133
Ameletus	0.082	0.05	5	4	26
Hydroptila	0.082	0.06	5	6	97
Nematoda	0.082	0.06	5	6	125
Hexatoma	0.082	0.03	5	2	88
Hydropsyche	0.083	0.06	5	5	232
Taenionema	0.083	0.04	5	3	29
Copepoda	0.084	0.07	5	6	35

Table B-1. Weighted-average indicator values for annual minima, 3-day means (continued)

3-Day annual minima					
Taxa	Optimum	Tolerance	Rank_opt	Rank_tol	Count
Microcylloepus	0.085	0.04	5	3	10
Leucotrichia	0.085	0.06	5	5	23
Chironomidae	0.085	0.07	5	6	291
Euparyphus	0.086	0.10	5	7	12
Isogenoides	0.086	0.04	6	2	19
Drunella	0.087	0.05	6	4	119
Dicranota	0.089	0.05	6	4	32
Tubificidae	0.090	0.06	6	5	107
Pteronarcys	0.090	0.03	6	1	27
Atherix	0.091	0.05	6	4	81
Planorbidae	0.091	0.08	6	7	37
Alisotrichia/Leucotricia	0.091	0.06	6	6	32
Micrasema	0.092	0.05	6	4	55
Brachycentrus	0.093	0.06	6	5	145
Hirudinea	0.094	0.09	6	7	75
Oligophlebodes	0.094	0.05	6	4	35
Forcipomyia/Probezzia	0.094	0.08	7	7	20
Agapetus/Culoptila/Protoptila	0.097	0.03	7	1	12
Pericoma	0.100	0.07	7	6	47
Bezzia	0.103	0.08	7	7	53
Helicopsyche	0.110	0.08	7	7	68
Hyalella	0.111	0.09	7	7	62
Traverella	0.116	0.03	7	1	10
Hesperophylax	0.159	0.08	7	7	12
Gammarus	0.170	0.07	7	6	15

Figures B-1 to B-4 show the ordination plots from the Nonmetric Multidimensional scaling (NMDS) and canonical correlation analysis (CCA).
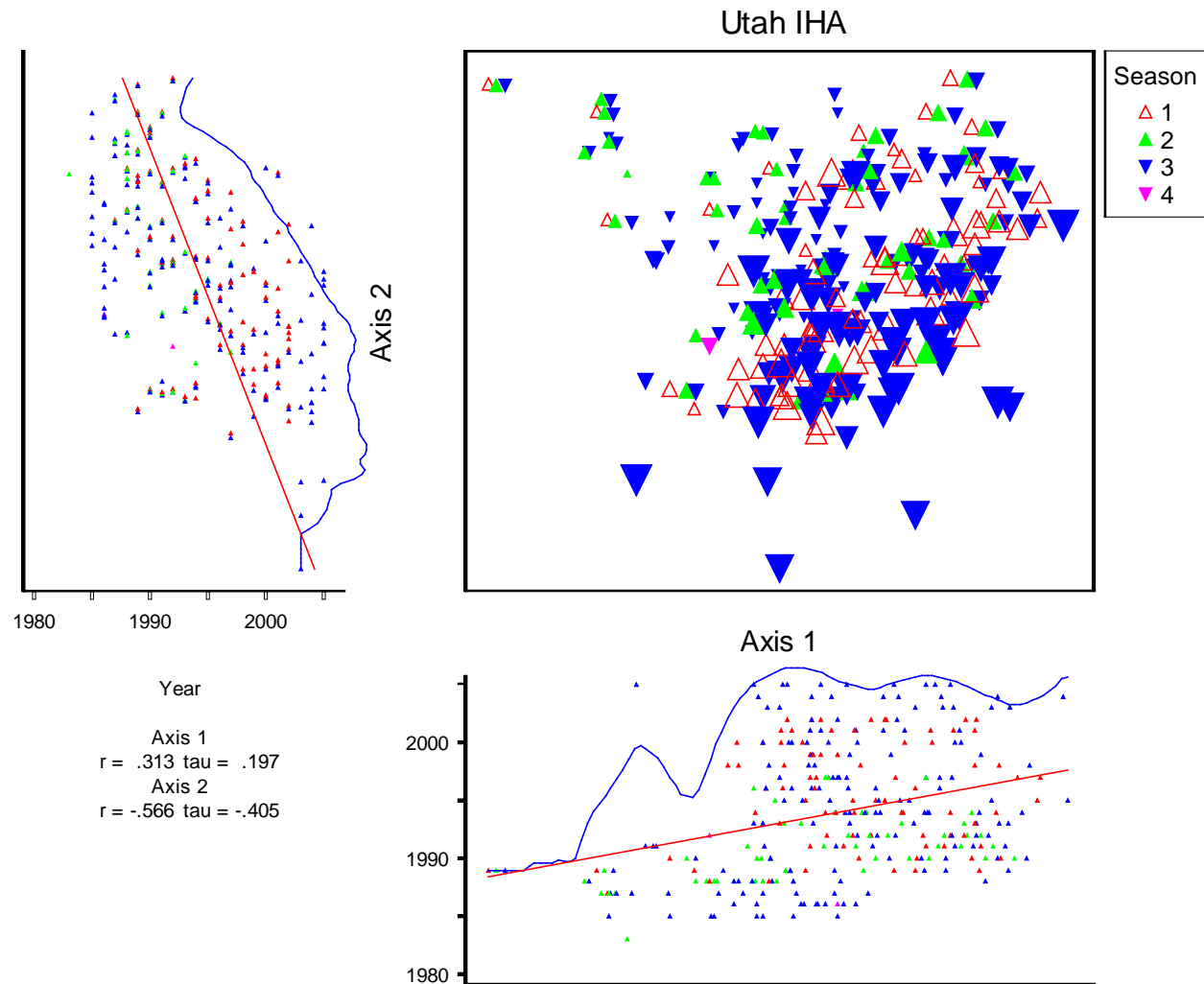
Figure B-2. Taxonomical trends in the Utah data set were examined using NMDS. Year had the strongest influence on taxonomical composition. However, when NMDS ordinations were run on a selected subset of data that only contained data from sites with multiple years of samples, the year trend was not as strong.
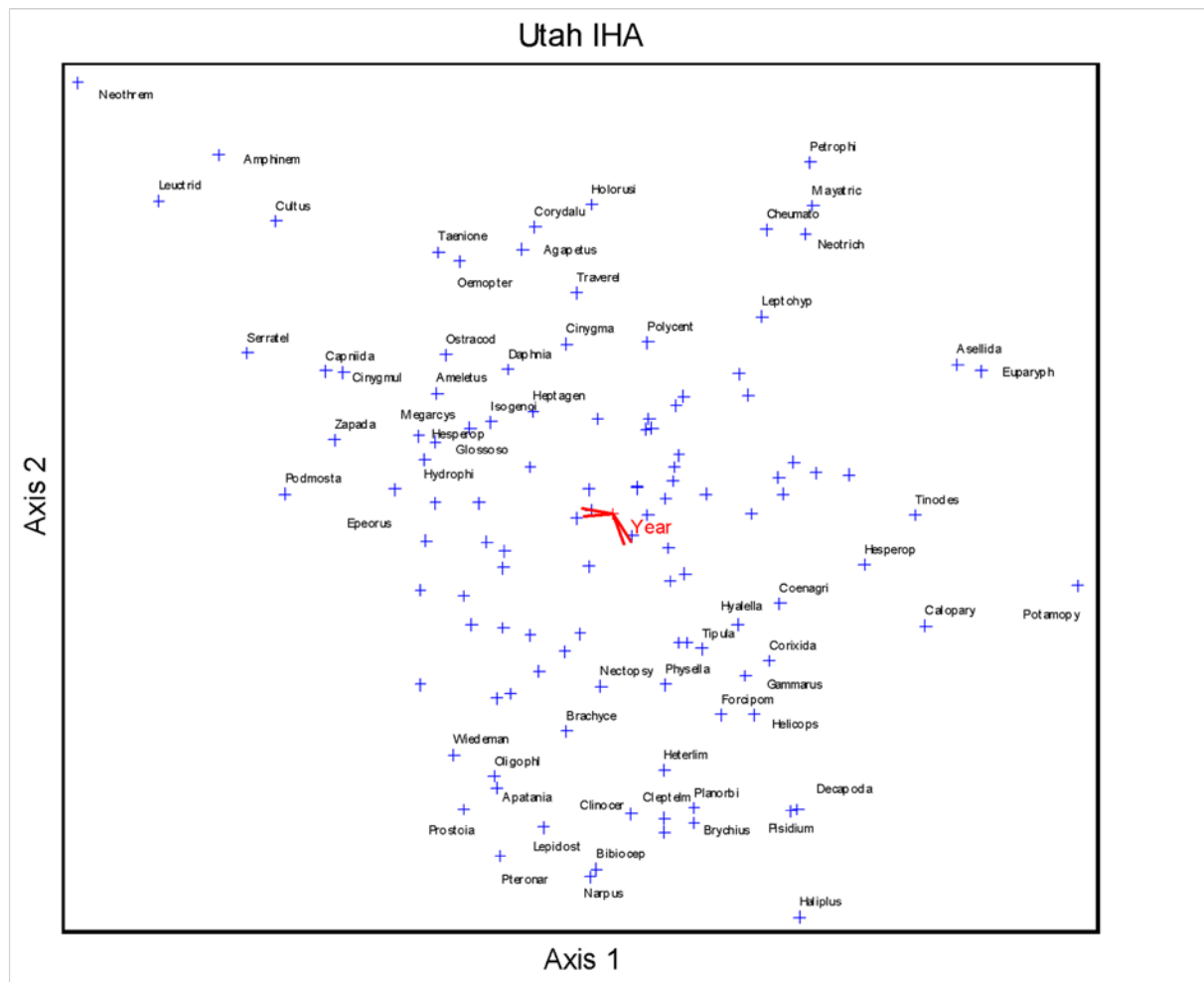
Figure B-3. Species trends along year. These were derived from the CCA analysis.
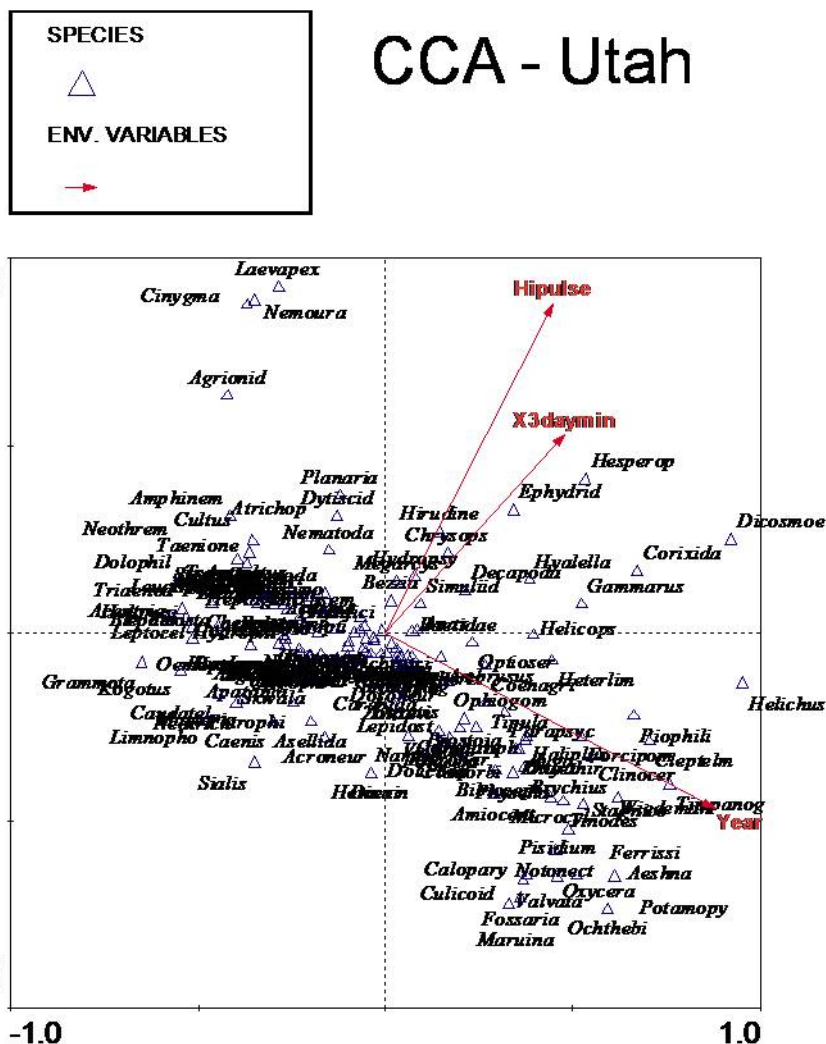
Figure B-4. CCA plot of a selected subset of the Utah biological-hydrological data.

Table B-2 shows a list of the Utah sites at which we ran correlation analyses.

B.2. 'EXTREME' ALTERATIONS OF UTAH FALL RIVPACS MODEL CLIMATE-RELATED PREDICTOR VARIABLE VALUES

We also ran some 'extreme' scenarios (i.e., doubling temperature, dividing precipitation values by two, changing freeze dates by 30 days, etc.) to explore how much the climate-related predictor variables would have to change in order to result in substantial changes to observed/expected (O/E) scores. Tables B-3 through B-8 show which scenarios were run and what the results were.

Table B-2. Data that were used in the Utah correlation analyses were gathered from these biological sampling stations/USGS gages. %URB = % urban, %AGR = % agricultural and %FOR = % forested land use within a 1-km buffer of the sites

BioStationID	USGS gage	# Years of data	Elev_ft	Eco_L3	Eco_L4	Ref status	%URB	%AGR	%FOR
4926350	10131000	14	5,573.3	Wasatch and Uinta Mountains	Mountain Valleys	TRASH	32.5	27.9	30.2
4934100	9302000	12	4,762.6	Colorado Plateaus	Uinta Basin Floor	UNKNOWN	3.9	18.4	24
4937900	9261000	14	4,766.1	Colorado Plateaus	Uinta Basin Floor	SO-SO	0	20.3	65.1
4954380	9330000	19	6,940.5	Wasatch and Uinta Mountains	Semiarid Foothills	TRASH	6.9	30.3	56
4996690	10163000	17	4,521.3	Central Basin and Range	Moist Wasatch Front Footslopes	TRASH	73.2	15.8	5.3
4998400	10154200	18	6,971.4	Wasatch and Uinta Mountains	Mid-elevation Uinta Mountains	SO-SO	5.7	0.7	93.6
5940440	10234500	11	6,249.3	Wasatch and Uinta Mountains	Semiarid Foothills	REF	3.9	0	96.1

Table B-3. Descriptions of how the climate-related predictor variables were altered in the 'extreme alteration' RIVPACS analyses

Run#	Category	Altered predictor variables	Rationale
1	Baseline	None—used original values	Get baseline values and quality control
2	Temperature	TMEAN.WS + 2 and TMEAN.NET + 2	National Center for Atmospheric Research (NCAR) annual temperature predictions (2050)
3		TMEAN.WS + 4 and TMEAN.NET + 4	NCAR annual temperature predictions (2090)
4		TMEAN.WS + 10 and TMEAN.NET + 10	Curiosity
5		TMEAN.WS + 20 and TMEAN.NET + 20	Curiosity
6	Precipitation	MEANP.PT − 0.05	NCAR annual precipitation predictions (2050)
7		MEANP.PT − 0.1	NCAR annual precipitation predictions (2090)
8		MEANP.PT − Minimum PRISM ppt14	Based on Parameter‑elevation Regressions on Independent Slopes Model (PRISM) ppt14 minimum values (1975−2006)
9		MEANP.PT/2	Curiosity
10		MINP.PT/2	Curiosity
11		MEANP.PT/2 and MINP.PT/2	Curiosity
12		MINWD.WS/2	Curiosity
13	Temperature and precipitation	TMEAN.WS + 2 and TMEAN.NET + 2 and MEANP.PT − 0.05	NCAR annual temperature and precipitation predictions (2050)
14		TMEAN.WS + 4 and TMEAN.NET + 4 and MEANP.PT − 0.1	NCAR annual temperature and precipitation predictions (2090)
15	Freeze date	LST32AVE − 2	Best professional judgment
16		LST32AVE − 5	Best professional judgment
17		FST32AVE + 5	Best professional judgment
18		LST32AVE − 5 and FST32AVE + 5	Best professional judgment
19		LST32AVE − 10	Curiosity
20		FST32AVE + 10	Curiosity
21		LST32AVE − 10 and FST32AVE + 10	Curiosity
22		LST32AVE − 15	Curiosity
23		LST32AVE − 15 and FST32AVE + 15	Curiosity

Table B-3. Descriptions of how the climate-related predictor variables were altered in the 'extreme alteration' RIVPACS analyses (continued)

Run#	Category	Altered Predictor variables	Rationale
24	Combine all	LST32AVE − 1, MINP.PT − 1, MEANP.PT − 1, TMEAN.NET + 1, TMEAN.WS + 1, FST32AVE + 1, MINWD.WS − 1	Best professional judgment
25		LST32AVE − 2, MINP.PT − 2, MEANP.PT − 2, TMEAN.NET + 2, TMEAN.WS + 2, FST32AVE + 2, MINWD.WS − 1	Best professional judgment

Table B-4. Results for the scenarios in which temperature predictor variables were altered

Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
			Baseline (original)			TMEAN.WS + 2 and TMEAN.NET + 2			
1	5940440	127636	14	15.09	0.93	14	14.92	0.94	0.01
7	4951200	120184	10	9.58	1.04	10	9.56	1.05	0
1	4936750	118524	15	14.04	1.07	15	14	1.07	0
6	4927250	127718	8	8.74	0.92	8	8.74	0.92	0

Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
			Baseline (original)			TMEAN.WS + 4 and TMEAN.NET + 4			
1	5940440	127636	14	15.09	0.93	14	14.8	0.95	0.02
7	4951200	120184	10	9.58	1.04	10	9.6	1.04	0
1	4936750	118524	15	14.04	1.07	15	14	1.07	0
6	4927250	127718	8	8.74	0.92	7	8.25	0.85	−0.07

Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
			Baseline (original)			TMEAN.WS + 10 and TMEAN.NET + 10			
1	5940440	127636	14	15.09	0.93	14	14.65	0.96	0.03
7	4951200	120184	10	9.58	1.04	10	9.61	1.04	0
1	4936750	118524	15	14.04	1.07	15	13.89	1.08	0.01
6	4927250	127718	8	8.74	0.92	7	8.24	0.85	−0.07

Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
			Baseline (original)			TMEAN.WS + 20 and TMEAN.NET + 20			
1	5940440	127636	14	15.09	0.93	13	14.08	0.92	0
7	4951200	120184	10	9.58	1.04	10	9.63	1.04	−0.01
1	4936750	118524	15	14.04	1.07	15	13.44	1.12	0.05
6	4927250	127718	8	8.74	0.92	7	8.24	0.85	−0.07

Table B-5. Results for the scenarios in which precipitation predictor variables were altered

			Baseline (original)			MEANP.PT − 0.05			
Group	**Site**	**Sample**	**O**	**E**	**O/E**	**O**	**E**	**O/E**	**Dif'ce O/E**
1	5940440	127636	14	15.09	0.93	14	15.1	0.93	0
7	4951200	120184	10	9.58	1.04	10	9.59	1.04	0
1	4936750	118524	15	14.04	1.07	15	14	1.07	0
6	4927250	127718	8	8.74	0.92	8	8.75	0.91	0

			Baseline (original)			MEANP.PT − 0.1			
Group	**Site**	**Sample**	**O**	**E**	**O/E**	**O**	**E**	**O/E**	**Dif'ce O/E**
1	5940440	127636	14	15.09	0.93	14	15.08	0.93	0
7	4951200	120184	10	9.58	1.04	10	9.58	1.04	0
1	4936750	118524	15	14.04	1.07	15	14.01	1.07	0
6	4927250	127718	8	8.74	0.92	8	8.74	0.92	0

			Baseline (original)			MEANP.PT − Min ppt14 PRISM			
Group	**Site**	**Sample**	**O**	**E**	**O/E**	**O**	**E**	**O/E**	**Dif'ce O/E**
1	5940440	127636	14	15.09	0.93	14	14.78	0.95	0.02
7	4951200	120184	10	9.58	1.04	10	9.51	1.05	0.01
1	4936750	118524	15	14.04	1.07	15	13.79	1.09	0.02
6	4927250	127718	8	8.74	0.92	8	8.71	0.92	0

			Baseline (original)			MEANP.PT/2			
Group	**Site**	**Sample**	**O**	**E**	**O/E**	**O**	**E**	**O/E**	**Dif'ce O/E**
1	5940440	127636	14	15.09	0.93	14	14.79	0.95	0.02
7	4951200	120184	10	9.58	1.04	10	9.43	1.06	0.02
1	4936750	118524	15	14.04	1.07	15	13.8	1.09	0.02
6	4927250	127718	8	8.74	0.92	8	8.68	0.92	0.01

Table B-5. Results for the scenarios in which precipitation predictor variables were altered (continued)

			Baseline (original)			MINP.PT/2			
Group	**Site**	**Sample**	**O**	**E**	**O/E**	**O**	**E**	**O/E**	**Dif'ce O/E**
1	5940440	127636	14	15.09	0.93	13	13.92	0.93	0.01
7	4951200	120184	10	9.58	1.04	10	9.46	1.06	0.01
1	4936750	118524	15	14.04	1.07	15	13.58	1.1	0.04
6	4927250	127718	8	8.74	0.92	8	8.69	0.92	0.01

			Baseline (original)			MEANP.PT/2 and MINP.PT/2			
Group	**Site**	**Sample**	**O**	**E**	**O/E**	**O**	**E**	**O/E**	**Dif'ce O/E**
1	5940440	127636	14	15.09	0.93	13	13.69	0.95	0.02
7	4951200	120184	10	9.58	1.04	10	9.33	1.07	0.03
1	4936750	118524	15	14.04	1.07	15	13.38	1.12	0.05
6	4927250	127718	8	8.74	0.92	8	8.16	0.98	0.07

			Baseline (original)			MINWD.WS/2			
Group	**Site**	**Sample**	**O**	**E**	**O/E**	**O**	**E**	**O/E**	**Dif'ce O/E**
1	5940440	127636	14	15.09	0.93	13	13.81	0.94	0.01
7	4951200	120184	10	9.58	1.04	10	9.53	1.05	0.01
1	4936750	118524	15	14.04	1.07	15	13.47	1.11	0.05
6	4927250	127718	8	8.74	0.92	7	7.63	0.92	0

Table B-6. Results for the scenarios in which both temperature and precipitation predictor variables were altered

Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
			Baseline (original)			TMEAN.WS + 2 and TMEAN.NET + 2 and MEANP.PT − 0.05			
1	5940440	127636	14	15.09	0.93	14	14.93	0.94	0.01
7	4951200	120184	10	9.58	1.04	10	9.56	1.05	0
1	4936750	118524	15	14.04	1.07	15	14.01	1.07	0
6	4927250	127718	8	8.74	0.92	7	8.24	0.85	−0.07
			Baseline (original)			TMEAN.WS + 4 and TMEAN.NET + 4 and MEANP.PT − 0.1			
1	5940440	127636	14	15.09	0.93	14	14.83	0.94	0.02
7	4951200	120184	10	9.58	1.04	10	9.58	1.04	0
1	4936750	118524	15	14.04	1.07	15	14.02	1.07	0
6	4927250	127718	8	8.74	0.92	7	8.26	0.85	−0.07

Table B-7. Results for the scenarios in which freeze date predictor variables were altered

Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
			Baseline (original)			**LST32AVE − 2**			
1	5940440	127636	14	15.09	0.93	14	15.05	0.93	0
7	4951200	120184	10	9.58	1.04	10	9.58	1.04	0
1	4936750	118524	15	14.04	1.07	15	14.01	1.07	0
6	4927250	127718	8	8.74	0.92	7	8.25	0.85	−0.07
			Baseline (original)			**LST32AVE − 5**			
1	5940440	127636	14	15.09	0.93	14	14.733	0.95	0.02
7	4951200	120184	10	9.58	1.04	10	9.5648	1.05	0
1	4936750	118524	15	14.04	1.07	15	13.999	1.07	0
6	4927250	127718	8	8.74	0.92	7	8.2433	0.85	−0.07
			Baseline (original)			**FST32AVE + 5**			
1	5940440	127636	14	15.09	0.93	15	15.374	0.98	0.05
7	4951200	120184	10	9.58	1.04	10	9.5875	1.04	0
1	4936750	118524	15	14.04	1.07	15	14.028	1.07	0
6	4927250	127718	8	8.74	0.92	8	8.7184	0.92	0
			Baseline (original)			**LST32AVE − 5 and FST32AVE + 5**			
1	5940440	127636	14	15.09	0.93	13	14.128	0.92	−0.01
7	4951200	120184	10	9.58	1.04	10	9.5647	1.05	0
1	4936750	118524	15	14.04	1.07	15	13.992	1.07	0
6	4927250	127718	8	8.74	0.92	7	8.224	0.85	−0.06
			Baseline (original)			**LST32AVE − 10**			
1	5940440	127636	14	15.09	0.93	13	14.02	0.93	0
7	4951200	120184	10	9.58	1.04	10	9.56	1.05	0
1	4936750	118524	15	14.04	1.07	15	13.7	1.09	0.03
6	4927250	127718	8	8.74	0.92	7	8.23	0.85	−0.07

Table B-7. Results for the scenarios in which freeze date predictor variables were altered (continued)

			Baseline (original)			FST32AVE + 10			
Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
1	5940440	127636	14	15.09	0.93	14	14.713	0.95	0.02
7	4951200	120184	10	9.58	1.04	10	9.6097	1.04	0
1	4936750	118524	15	14.04	1.07	15	13.797	1.09	0.02
6	4927250	127718	8	8.74	0.92	7	8.1843	0.86	−0.06
			Baseline (original)			LST32AVE − 10 and FST32AVE + 10			
Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
1	5940440	127636	14	15.09	0.93	13	13.743	0.95	0.02
7	4951200	120184	10	9.58	1.04	10	9.6115	1.04	0
1	4936750	118524	15	14.04	1.07	15	13.532	1.11	0.04
6	4927250	127718	8	8.74	0.92	7	8.1706	0.86	−0.06
			Baseline (original)			LST32AVE − 15			
Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
1	5940440	127636	14	15.09	0.93	13	13.945	0.93	0
7	4951200	120184	10	9.58	1.04	10	9.5818	1.04	0
1	4936750	118524	15	14.04	1.07	15	13.454	1.11	0.05
6	4927250	127718	8	8.74	0.92	7	8.2214	0.85	−0.06
			Baseline (original)			LST32AVE − 15 and FST32AVE + 15			
Group	Site	Sample	O	E	O/E	O	E	O/E	Dif'ce O/E
1	5940440	127636	14	15.09	0.93	13	13.415	0.97	0.04
7	4951200	120184	10	9.58	1.04	10	9.6052	1.04	0
1	4936750	118524	15	14.04	1.07	14	12.787	1.09	0.03
6	4927250	127718	8	8.74	0.92	7	8.1713	0.86	−0.06

Table B-8. Results for scenarios in which combinations of all climate-related predictor variables were altered simultaneously

Group	Site	Sample	Baseline (original)			Changed by 1			
			O	E	O/E	O	E	O/E	Dif'ce O/E
1	5940440	127636	14	15.09	0.93	13	14.04	0.93	0
7	4951200	120184	10	9.58	1.04	10	9.51	1.05	0.01
1	4936750	118524	15	14.04	1.07	15	14.03	1.07	0
6	4927250	127718	8	8.74	0.92	8	8.71	0.92	0
			Baseline (original)			Changed by 2			
			O	E	O/E	O	E	O/E	Dif'ce O/E
1	5940440	127636	14	15.09	0.93	13	13.81	0.94	0.01
7	4951200	120184	10	9.58	1.04	10	9.49	1.05	0.01
1	4936750	118524	15	14.04	1.07	15	14.03	1.07	0
6	4927250	127718	8	8.74	0.92	7	8.23	0.85	−0.06

APPENDIX C

MAINE DECISION MODEL AND ANALYSES ON COMPONENT METRICS

C.1. OVERVIEW OF MAINE'S DEPARTMENT OF ENVIRONMENTAL PROTECTION (ME DEP) AQUATIC LIFE DECISION MODELS AND SAMPLE VARIABLES (PROVIDED BY MAINE DEP)

ME DEP's aquatic life decision models are four statistical models that use 30 variables of the macroinvertebrate community to determine the strength of association of a sample community to Maine's water quality classes. Each of the four linear discriminant models uses different variables, providing independent estimates of class membership. Association values are computed for each classification using one 4-way model and three 2-way models. The protocol is outlined in the ME DEP methods manual (Davies and Tsomides, 2002).

C.1.1. First-Stage Model and Variables

The first-stage model acts as a screen and gives the strength of association of the sample to each of the different water quality classes. This model provides four initial probabilities that a given site attains one of three classes (A, B, or C) or is in nonattainment (NA) of the minimum criteria for any class. These probabilities have a possible range from 0.0 to 1.0 and, after transformation, they are used as variables in each of the three subsequent second-stage or final decision models. See the section below on second-stage models.

The variables used in the first-stage model are variables important to the evaluation of all classes. Of the nine variables used in the first modeling stage, five measure abundance, two measure richness, and two variables are biotic indices involving tolerance to pollution and abundance. The **first-stage model** uses the following nine variables:

1. **Total Mean Abundance**—Total mean abundance (the mean number of individuals in a sample, usually based on 3 replicates) is a basic measure of community structure and is a strong predictor of both Class A and nonattainment. Total abundance values for the water quality classes appear to follow a curve shaped like the Odum et al. (1979) subsidy-stress gradient. Values for Class A are relatively low, due to low nutrients in natural Maine waters. Values for Class B and C communities tend to be high, indicating increased resources that might be available in a waterbody with increased loadings of materials from human alterations. Abundance values in nonattainment waters tend to be low but can also be highly variable.

2. **Generic Richness**—Richness (total number of taxa in a sample) is a good measure of water quality impact, declining as water quality declines. Low richness is a good predictor of nonattainment. Like abundance, richness follows the generalized subsidy-stress curve.

3. **Plecoptera Mean Abundance**—Plecoptera, or stoneflies, are very intolerant of even mild levels of pollution. Abundance is highest for Class A and declines with the classes to be nearly absent from the nonattainment class. The Maine water quality classification requires that Class A and B waters support all indigenous species, so it is expected that Plecoptera numbers will be maintained in those classes. Stoneflies function as predators and shredders.

4. **Ephemeroptera Mean Abundance**—Ephemeroptera, or mayflies, are intolerant of many pollutants, so abundances are distinctly lower for nonattainment samples than the other classes. Mayflies function as scrapers and collectors. Together with the stoneflies, these two groups represent highly sensitive orders that fulfill the major functional feeding roles in the community. These orders are important components of a Class A or B community.

5. **Shannon-Wiener Generic Diversity** (Shannon and Wiener, 1963)—Diversity is composed of a richness factor and an evenness factor. Richness distributes between the classes along a subsidy-stress curve. Diversity shows a decline in value from Class A to the nonattainment class as certain pollution-tolerant taxa gain advantages, due to increasing pollution load or other activities. As both diversity and richness decline, the stability of most natural communities usually declines.

6. **Hilsenhoff Biotic Index** (Hilsenhoff, 1987)—The biotic index provides a measure of the general tolerance level of the sample community toward organic (nutrient) enrichment. The index increases in value from Class A to the nonattainment class, indicating that increases in abundance may be attributable to increases among the tolerant taxa (a change allowed in Class B or C), or that there may be a decline in the taxa pool of intolerant organisms (a change allowed in Class C).

7. **Relative Chironomidae Abundance**—Chironomidae, a Family of flies in the Order Diptera that includes Nonbiting Midges and Midges, consist of a great number of taxa with wide-ranging tolerances and adaptations. Many tend to increase with increasing pollution load, probably as a response to reduced competition and predation, and to increased organic matter supply. Many have very short generation times and are, thus, capable of quickly colonizing areas where these conditions exist. The taxa that cause these increases are the collector types adapted to feeding on fine organic matter; some are primarily predators. These genera have been observed to increase in relative abundance presumably because of tolerance to reduced water quality, particularly the presence of some toxic substances, and the availability of other pollution tolerant prey.

8. **Relative Diptera Richness**—Many Diptera, or true flies, are pollution tolerant organisms. Relative Diptera richness increases from Class A to the nonattainment class. Increases in Diptera, particularly Chironomidae, have been observed with increasing pollution and sedimentation and loss of Ephemeroptera, Plecoptera, and Trichoptera.

9. *Hydropsyche* **Mean Abundance**—The genus *Hydropsyche*, one of the common net-spinning Caddisflies, provides some added discrimination to the model. Higher values for *Hydropsyche* abundance are found for Class B and are nearly absent from

nonattainment samples. *Hydropsyche* is a filter feeder and prospers under conditions of mild enrichment of suspended organic particles, conditions that might naturally be found below a lake outlet or might be found in Class B waters below a treatment plant outfall or in the presence of nutrient enrichment from nonpoint source pollution activities (e.g., agriculture). Relative to other genera of the Hydropsychidae family, *Hydropsyche* is usually less tolerant of low dissolved oxygen or toxic substances.

C.1.2. Second-Stage Models and Variables

The final decision models (the three, two-way models) are designed to distinguish between a given class and any higher classes as one group and any lower classes as another group (e.g., Classes A + B + C vs. NA; Classes A + B vs. Class C + NA; Class A vs. Classes B + C + NA). The equations for the final decision models use the predictor variables relevant to the class being tested. The process of determining attainment class using the association value is outlined in Appendix F of the ME DEP methods manual (Davies and Tsomides, 2002). Application of the three second-stage models or two-group tests is hierarchical:

"C or better" model: The first second-stage model determines the probability that an unknown sample belongs in the cluster of samples A + B + C versus the probability that it belongs in the cluster of nonattainment of Class C samples. This is referred to as the "C or better" model, which determines if the sample is at least a Class C, using the following variables:

1. **Probability (A + B + C)** from First-stage Model

2. *Cheumatopsyche* **Mean Abundance**—The abundance of *Cheumatopsyche*, one of the common net-spinning Caddisflies, generally increases with declining water quality and is usually the last of the Ephemeroptera-Plecoptera-Trichoptera genera found in abundance as water quality declines because *Cheumatopsyche* are generally found to be the most pollution tolerant genera within the family Hydropsychidae, among the order Trichoptera.

3. **Ephemeroptera, Plecoptera, Trichoptera (EPT)—Diptera Richness Ratio**—(uses all Diptera rather than just the Chironomidae.). Ephemeroptera-Plecoptera-Trichoptera are usually poorly represented in communities where water quality is poor. These orders provide considerable functional variety to aquatic communities, and when severely depleted, or replaced by Diptera, signal dysfunction of the community. Maine data show distinct separation of values for this variable between Class A, B, and C communities and the nonattainment communities.

4. **Relative Oligochaeta Abundance**—Proliferation of Oligochaeta, aquatic worms, has long been recognized as an indication of polluted waters, because many taxa are highly tolerant of low oxygen conditions and certain toxic substances, feed on fine organic particles and can colonize quickly in the absence of predators. Communities dominated by Oligochaeta are found when pollution loads are excessive. These organisms are usually the last to be eliminated by pollutant overloading and as the relative abundance of Oligochaeta increases, community structure, and function are usually diminished.

"B or better" model: The second two-way model is the "B or better" model, which determines if the unknown sample attains at least Class B standards. It discriminates between the cluster of A + B samples and the cluster of C + nonattainment of Class C samples. Family functional groups are important in this second two-way model. Changes in functional feeding group composition indicate the energy pathways through the aquatic ecosystem have been significantly altered. The major functional groups in the Maine data are as follows: collector-filterer, collector-gatherer, piercer, predator, scraper, and shredder. The "B or better" model uses the following variables:

1. **Probability (A + B)** from First-stage Model

2. **Perlidae Mean Abundance** (Family Functional Group)—Greater abundance of this family functional group is expected to occur in higher quality waters. This family of stoneflies encompasses large predators and usually occurs in waters of good quality. Generation time for some of these taxa is greater than 1 year; therefore, populations will persist only where water quality is consistently good for long periods of time.

3. **Tanypodinae Mean Abundance** (Family Functional Group)—This subfamily functional group is usually found in greater abundance in waters of lower quality. This Chironomidae subfamily is also a predator group, but these organisms are small in comparison to the Perlidae, and feed on small Oligochaeta and other Chironomidae that can also tolerate lower water quality.

4. **Chironomini Mean Abundance** (Family Functional Group)—Greater abundance of this Chironomidae subfamily group indicates increased availability of organic matter. Many taxa in this group are known to tolerate lower water quality. These organisms are collector-gatherers favoring fine, settled organic particles. Many of these taxa are multivoltine, capable of quickly colonizing favorable habitats and recolonizing after disturbances.

5. **Relative Ephemeroptera Abundance**—The Ephemeroptera, or mayflies, are generally an intolerant order and tend to be indicators of good to excellent water quality. While total Ephemeroptera abundance was used as a discriminating variable in the second-stage

discriminant model to separate the four classes, relative abundance is used to separate these two groups, particularly between the Class B and C waters. While Ephemeroptera abundance may not decline appreciably in Class C waters, there is an expectation for other non-Ephemeroptera taxa to increase.

6. **EPT Generic Richness**—EPT richness has been a common measure to identify waters of good quality. Of the three orders, Ephemeroptera and Plecoptera are considered the more intolerant. Many of the Trichoptera are also intolerant of low water quality. Collectively, these orders have a wide array of functional characteristics (feeding strategies and preferred resources, reproductive and life cycle strategies, habitat preferences). Higher values for EPT richness are indicative of a structurally and functionally diverse community. As EPT richness diminishes, it is presumed that this functional diversity also declines.

7. **Sum of Mean Abundances of *Dicrotendipes, Micropsectra, Parachironomus,* and *Helobdella***—The sum of the abundance of four indicator taxa (three Chironomidae genera and one leech genera) is also used. All four are detritivores and generally occur in abundance only when water quality is diminished. A high abundance of this group is indicative of conditions of Class C or nonattainment.

"Class A" model: Class A is the highest quality water and is expected to be supportive of natural populations with the expectation that the community include many pollutant-intolerant organisms. The Class A decision model relies on the probability score from the second-stage linear discriminant function and many indicator taxa to ascertain Class A quality. The third two-way model is the "Class A" model and discriminates Class A samples from the cluster of samples in Classes B + C + Nonattainment of Class C using the following variables:

1. **Probability of Class A** from First-stage Model

2. **Relative Plecoptera Richness**—Plecoptera are well known as an intolerant order, showing great intolerance to a variety of pollutants. Their reproductive strategies render them slow to recolonize areas where they have been eliminated. Water quality, therefore, needs to be consistently good for the Plecoptera to be present. Relative richness of Plecoptera is expected to be greatest in the highest quality waters.

3. **Sum of Mean Abundance of *Cheumatopsyche*, *Cricotopus*, *Tanytarsus*, and *Ablabesmyia***—These four taxa (a net-spinning Caddisfly and three Chironomidae genera) are considered pollution-tolerant and are not expected to occur in abundance in Class A waters. All four taxa occur most commonly in lower quality waters and may replace functions of less tolerant organisms when those populations decline.

4. **Sum of Mean Abundances of *Acroneuria* and *Stenonema*—***Acroneuria* (a stonefly genera of the Perlidae Family) and *Stenonema* (a mayfly genera) are two of the most common and abundant taxa in their respective orders and indicators of good water quality. The sum of their abundance provides a good discriminating variable.

5. **Ratio of Ephemeroptera and Plecoptera (EP) Generic Richness—**EPT richness is a good discriminating variable to identify Class A and B waters, but of this group, the Ephemeroptera and Plecoptera were usually the less tolerant taxa of the three orders. EPT richness is, thus, used as a variable for Class A waters.

6. **Ratio of Class A Indicator Taxa**—The number of Class A indicators divided by 7 (which is the total number possible). Seven indicator taxa were identified for Class A communities. Class A indicator taxa were present in 100% of Class A communities, <26% of Class B communities, <16% of Class C communities, and <1% of nonattainment communities. Class A indicator taxa were rarely found to be dominant taxa except in Class A communities. Values of zero for this variable (# of Class A indicator taxa among 5 most dominant taxa) were found in sample communities that were not determined to support Class A conditions. Class A communities had one or more indicator taxa among the five most dominant taxa for 54% of the samples. The Class A indicators are *Brachycentrus* (Trichoptera: Brachycentridae), *Serratella* (Ephemeroptera: Ephemerellidae), *Leucrocuta* (Ephemeroptera: Heptageniidae), *Glossosoma* (Trichoptera: Glossosomatidae), *Paragnetina* (Plecoptera: Perlidae), *Eurylophella* (Ephemeroptera: Ephemerellidae), and *Psilotreta* (Trichoptera: Odontoceridae).

Figure C-1 shows a flow chart that depicts Maine DEP's decision criteria. The protocol is also outlined in the Maine DEP methods manual (i.e., Davies and Tsomides, 2002).

Process for Determining Attainment Class Using Association Values

Is the sample appropriate for LDM?

YES — NO

BPJ[1]

Is the sample class C or better?

pABC ≥ 0.6 | 0.4 ≤ pABC < 0.6 | pABC < 0.4

At least C | At least C | Indeterminate | NA | NA

Is the sample class B or better?

pAB ≥ 0.6 | 0.4 ≤ pAB < 0.6 | pAB < 0.4

At least B | At least B | Indeterminate | C | C

Is the sample class A?

pA ≥ 0.6 | 0.4 ≤ pA < 0.6 | pA < 0.4

A | A | Indeterminate | B | B
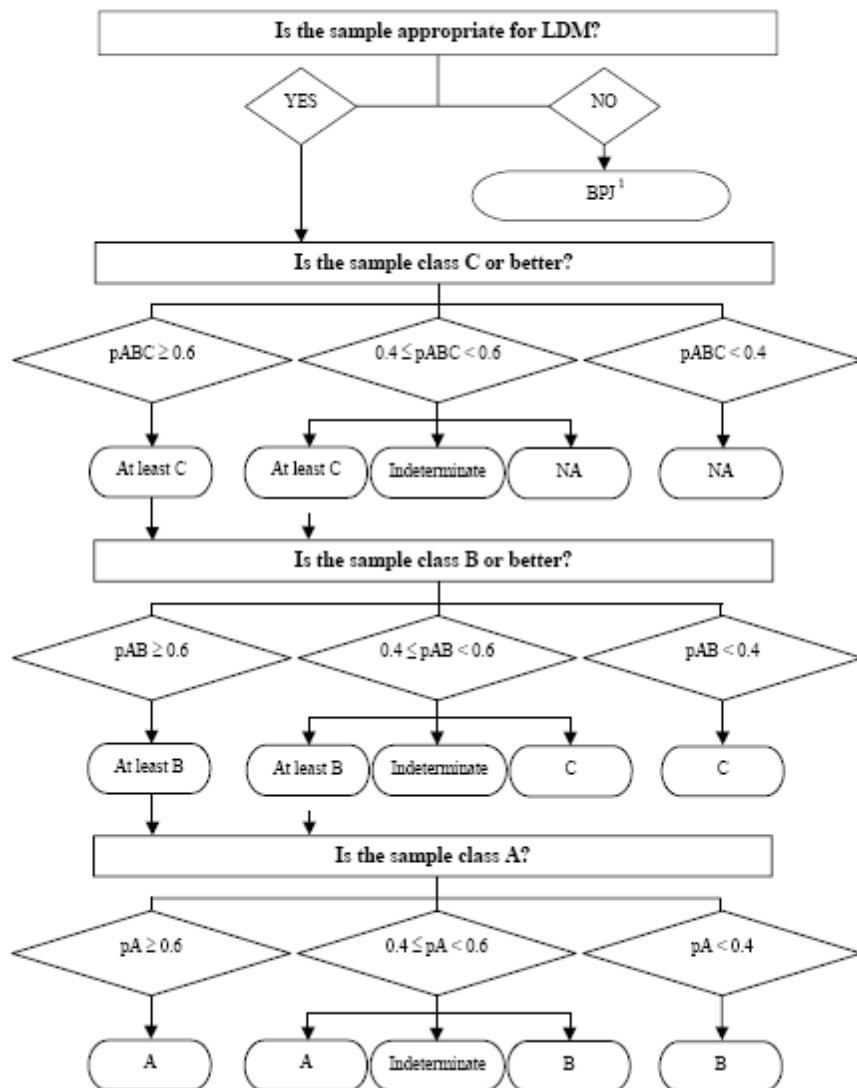
Figure C-1. Flow chart that outlines the process that Maine DEP uses for determining attainment class using association values from its four linear discriminant models (chart by Thomas J. Danielson, taken from ME DEP 2002 monitoring manual).

C.2. BOX PLOTS SHOWING THE DISTRIBUTIONS OF THE MODEL INPUT METRICS ACROSS THE DIFFERENT CLASSIFICATION GROUPS

Figures C-2 through C-24 show categorical box-and-whisker plots showing distributions of mean model input metric values across the classification groups based on a data set composed of rock-basket or rock-cone samples collected during Maine DEP's July−September index period.
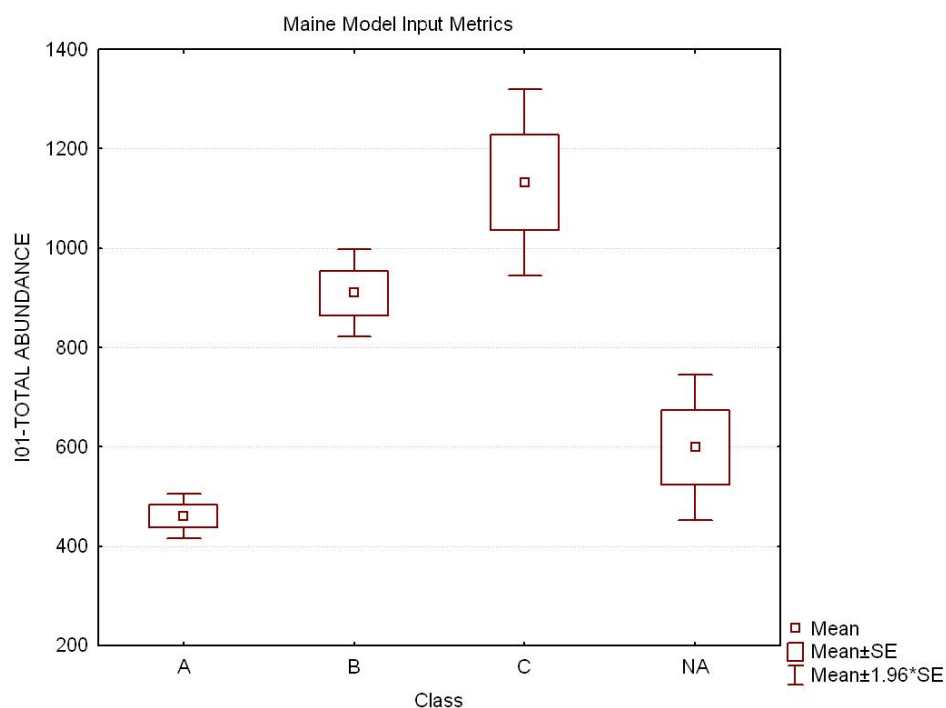
Figure C-2. Differences in total taxa abundance by class showing mean and standard error (SE).
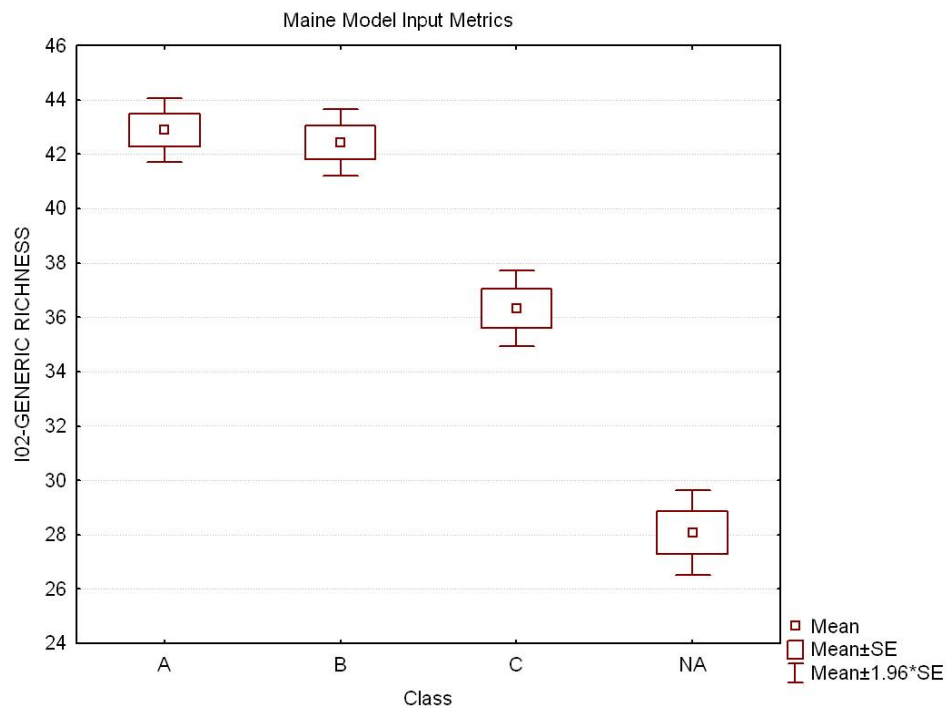
Figure C-3. Differences in richness of genera by class.
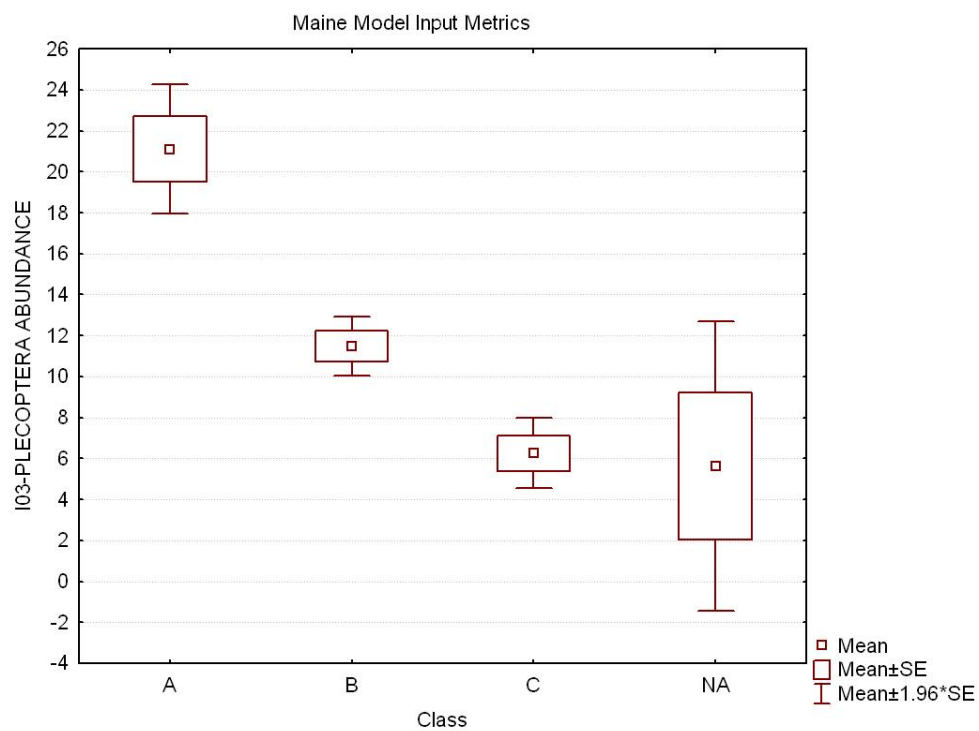
Figure C-4. Differences in Plecoptera abundance by class.
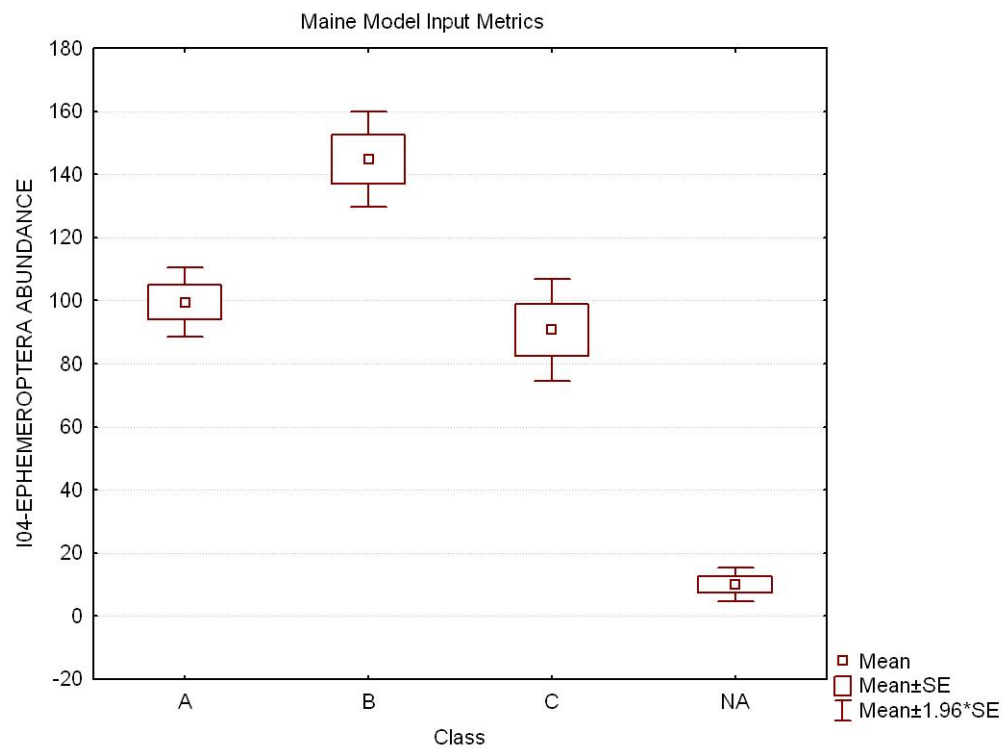
Figure C-5. Differences in Ephemeroptera abundance by class.
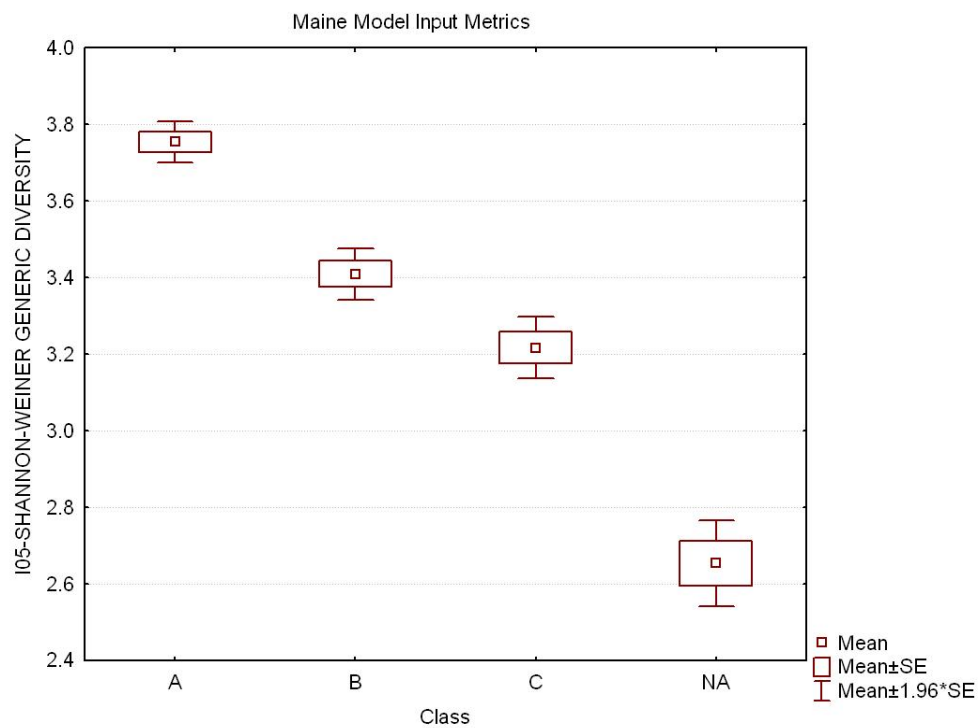
Figure C-6. Differences in Shannon-Wiener diversity of genera by class.
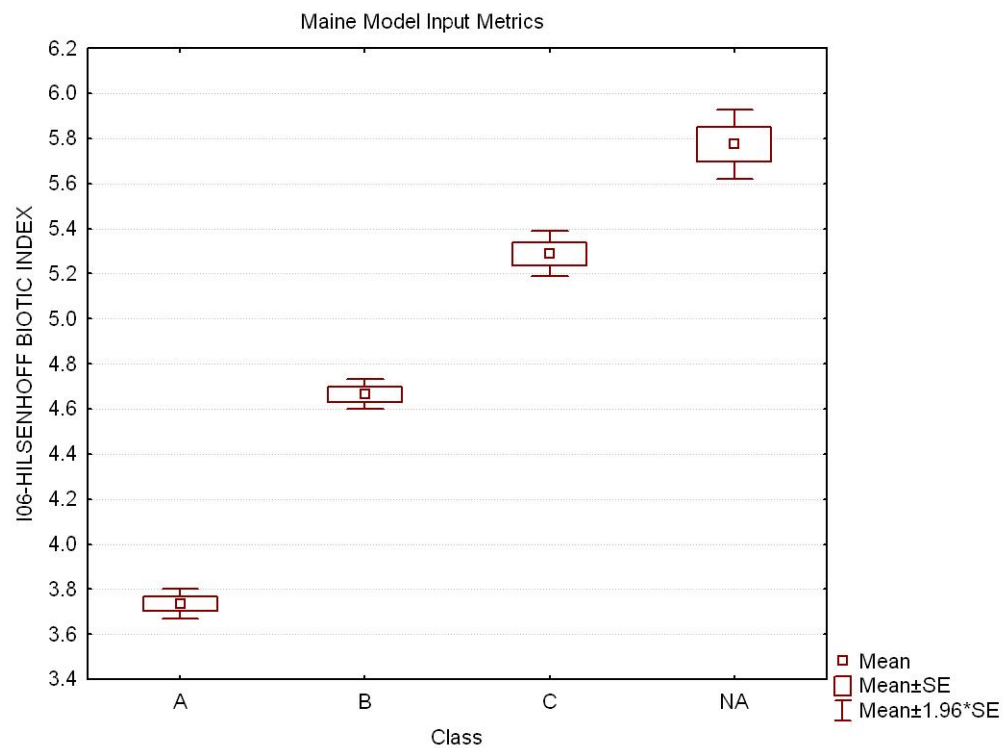
Figure C-7. Differences in Hilsenhoff Biotic Index by class.
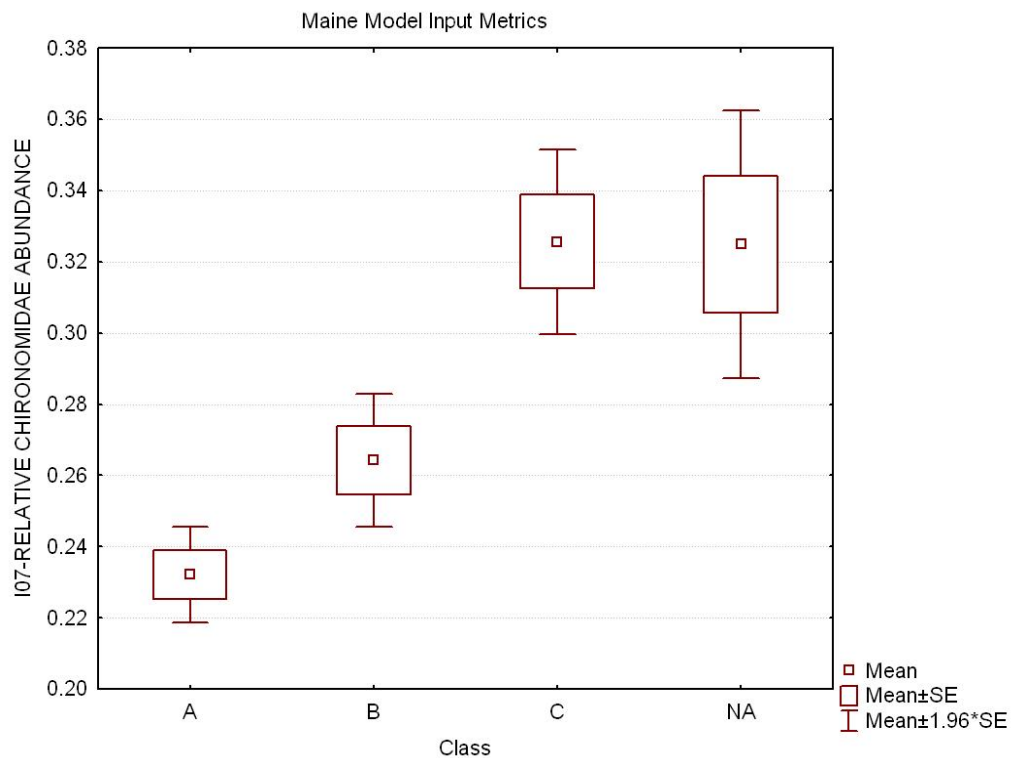
Figure C-8. Differences in relative Chironomid abundance by class.

C-12
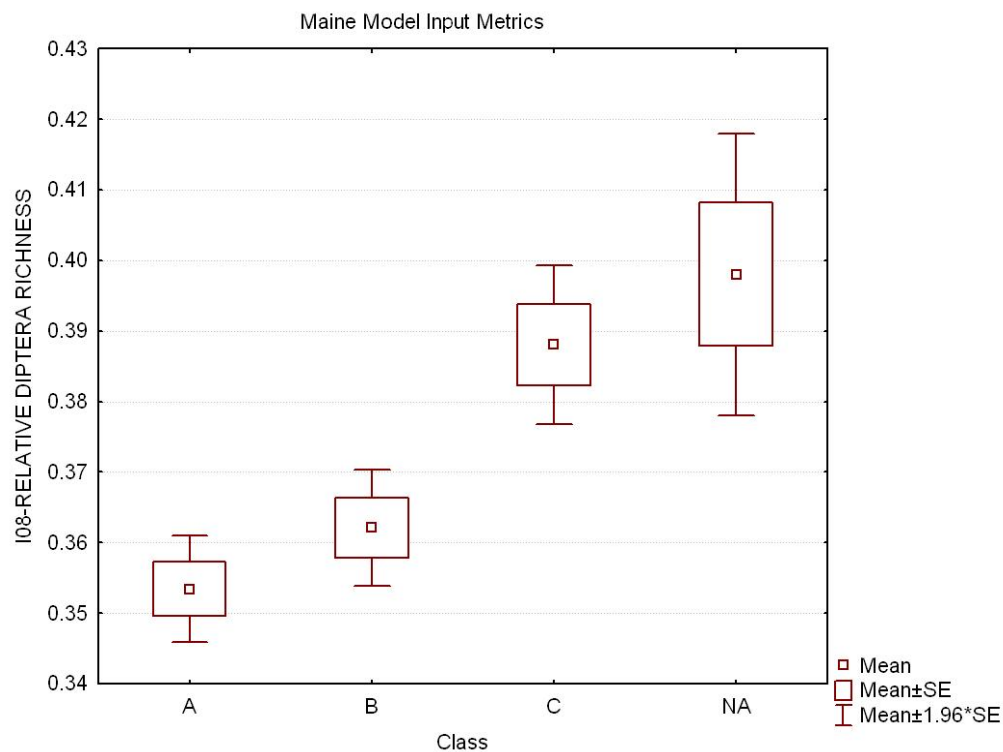
Figure C-9. Differences in relative Diptera richness by class.
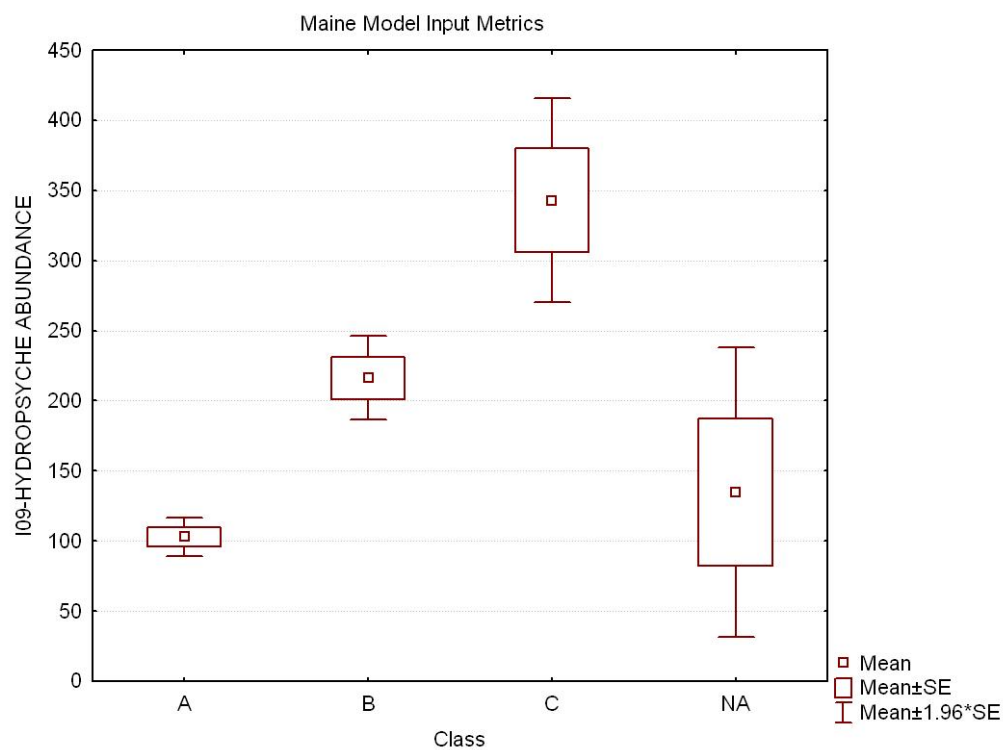
Figure C-10. Differences in *Hydropsyche* abundance by class.
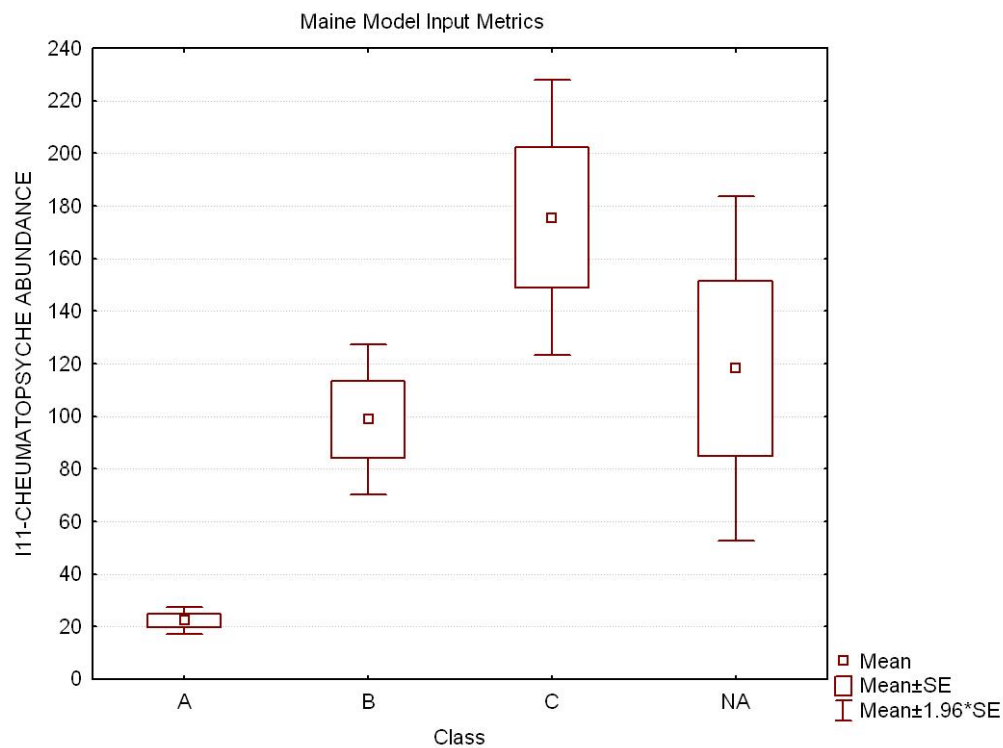
Figure C-11. Differences in *Cheumatopsyche* abundance by class.
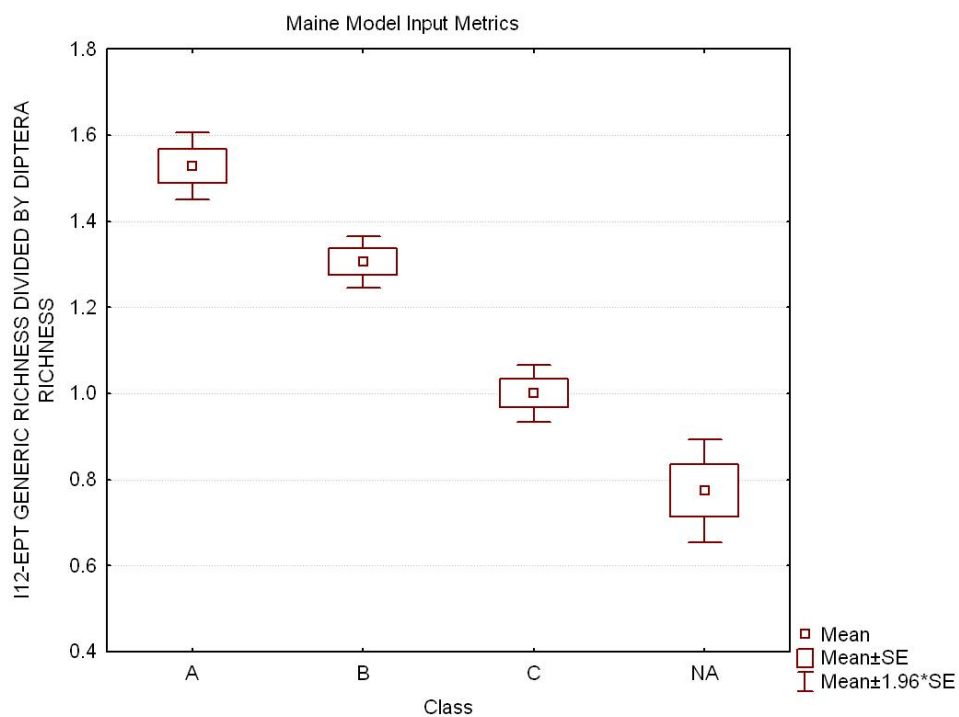
Figure C-12. Differences in EPT richness over diptera richness by class.
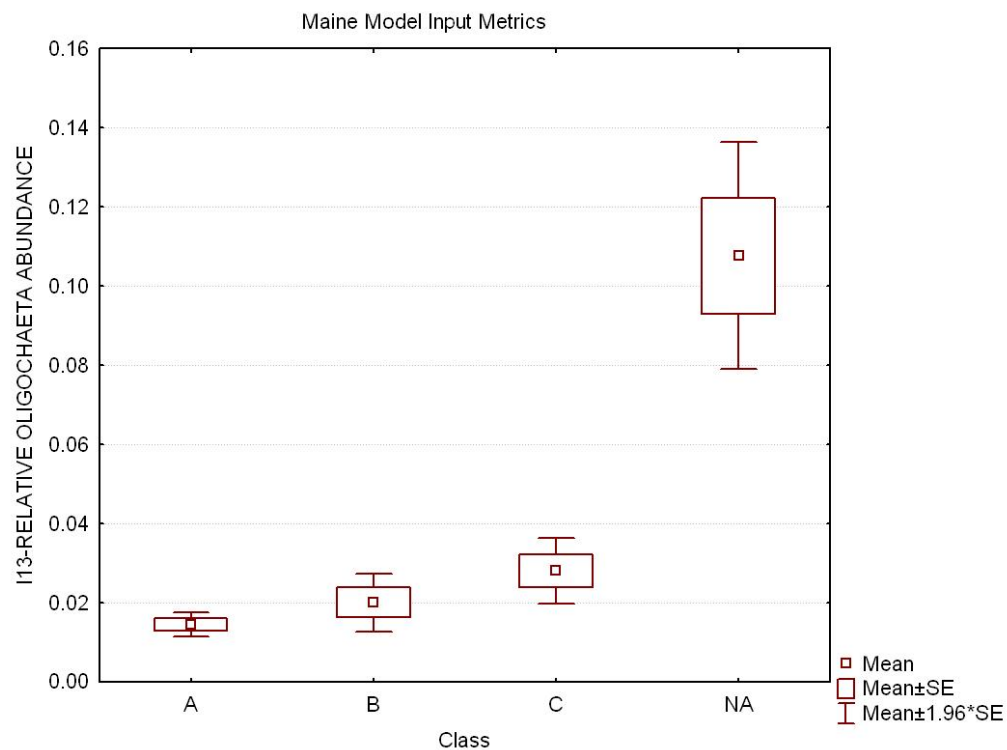
Figure C-13. Differences in relative Oligochete abundance by class.
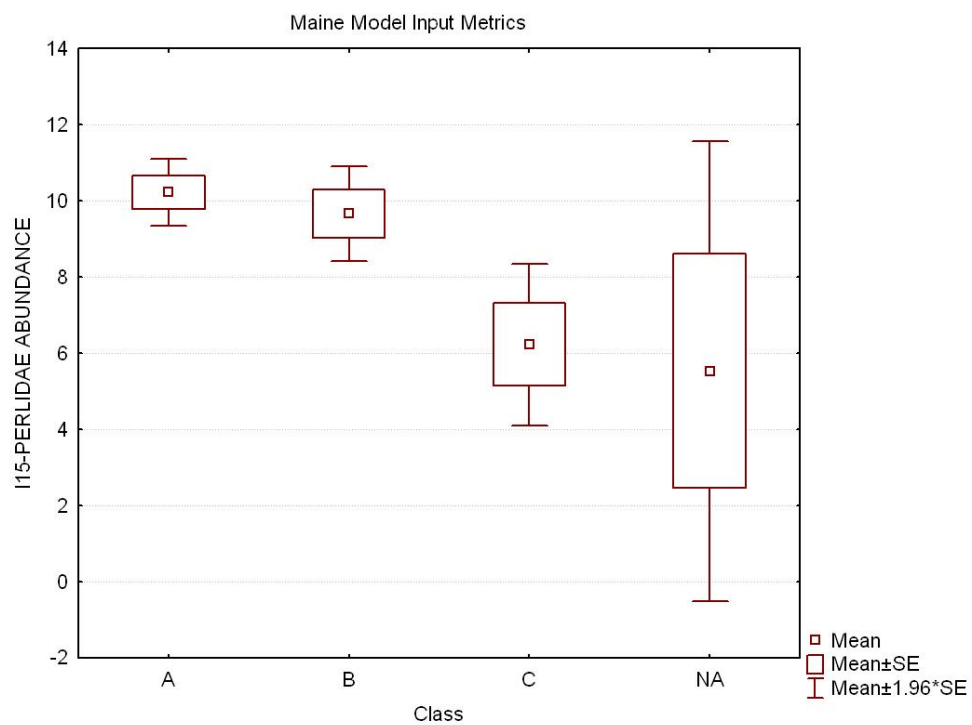
Figure C-14. Differences in Perlidae abundance by class.

C-15
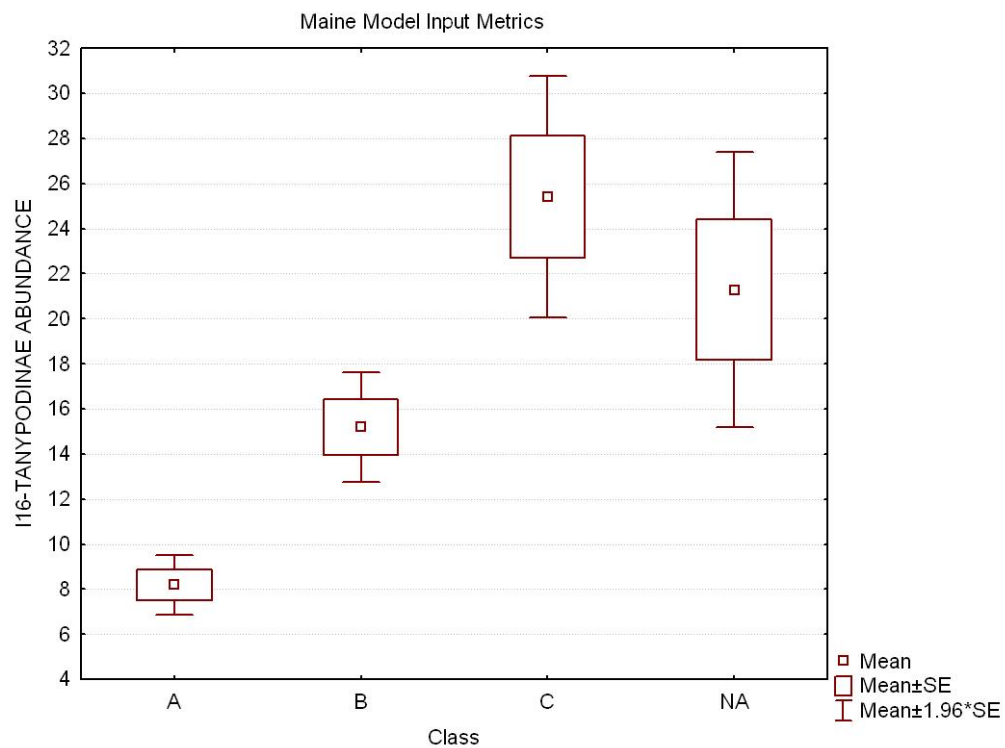
Figure C-15. Differences in Tanypodinae abundance by class.
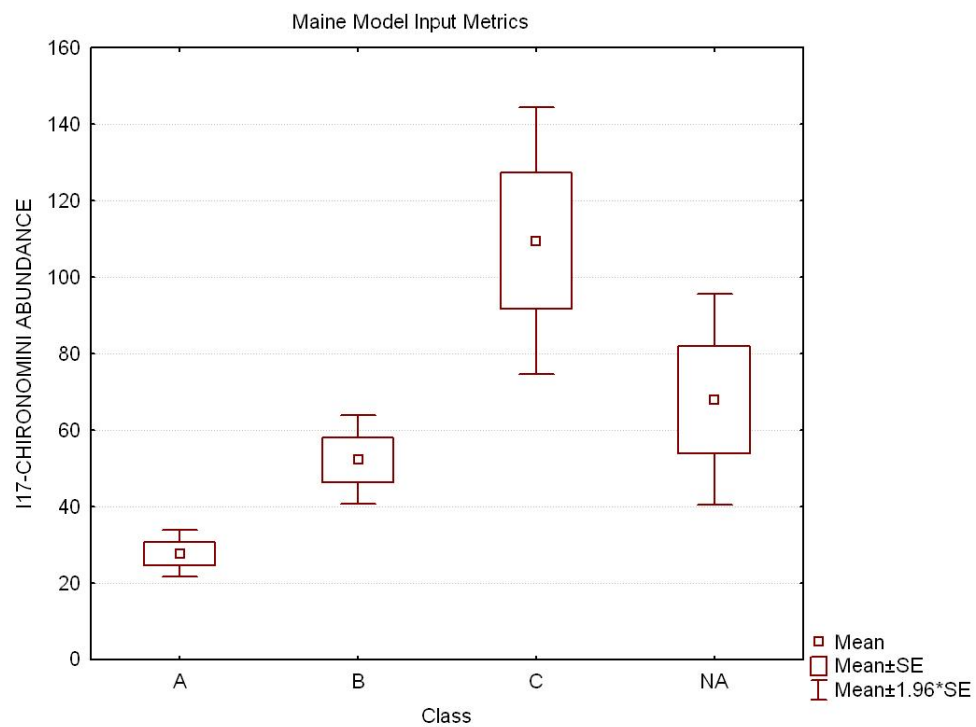
Figure C-16. Differences in Chironomid abundance by class.
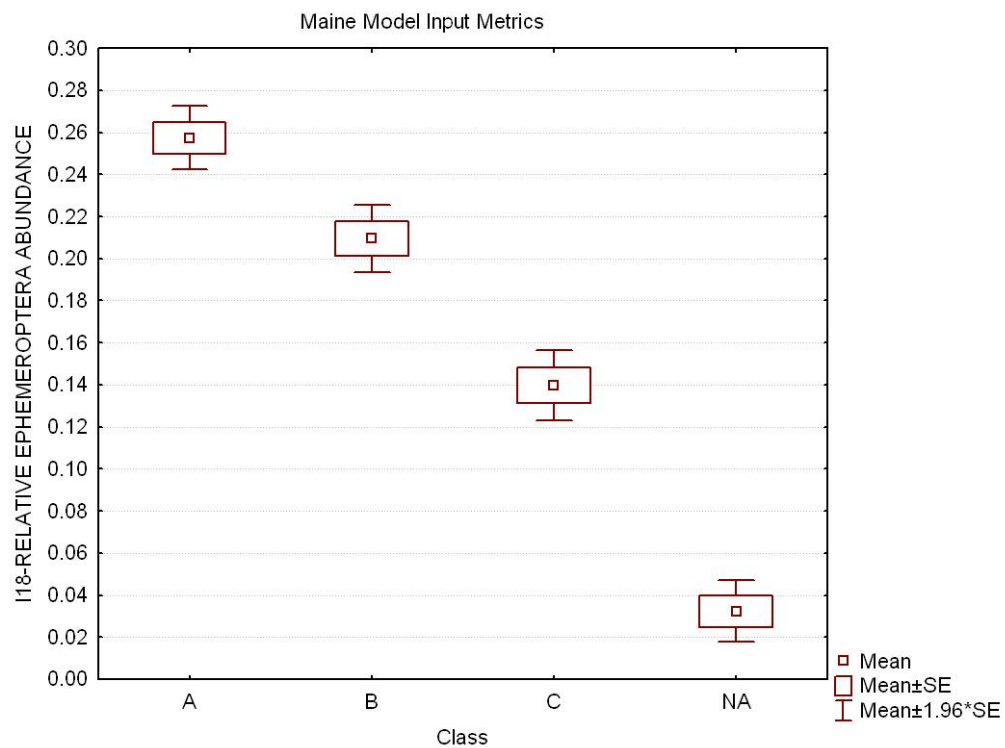
Figure C-17. Differences in relative Ephemeroptera abundance by class.
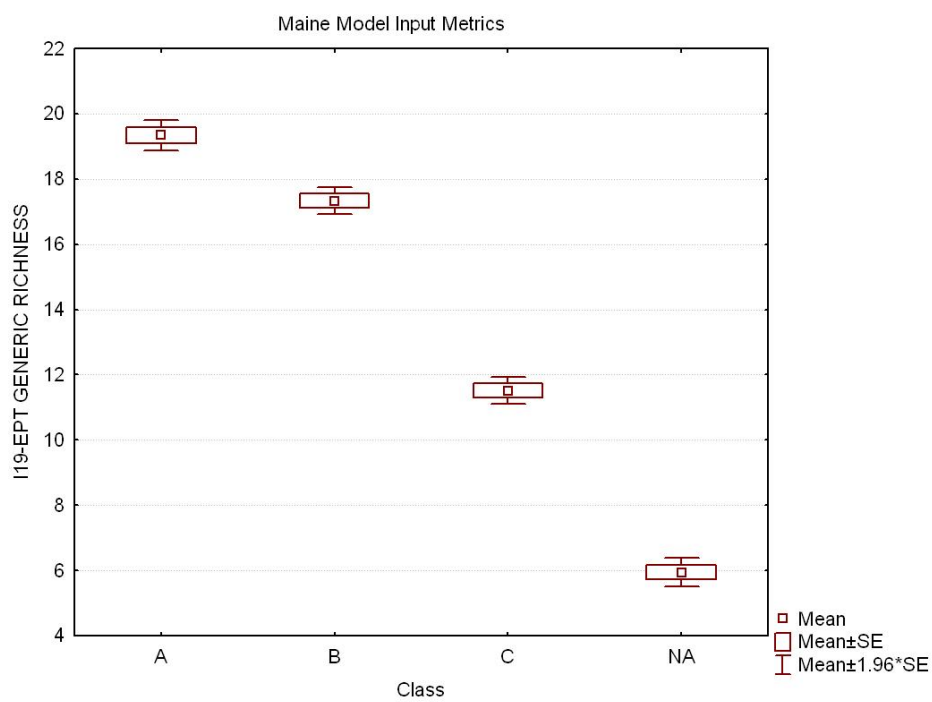
Figure C-18. Differences in EPT richness by class.
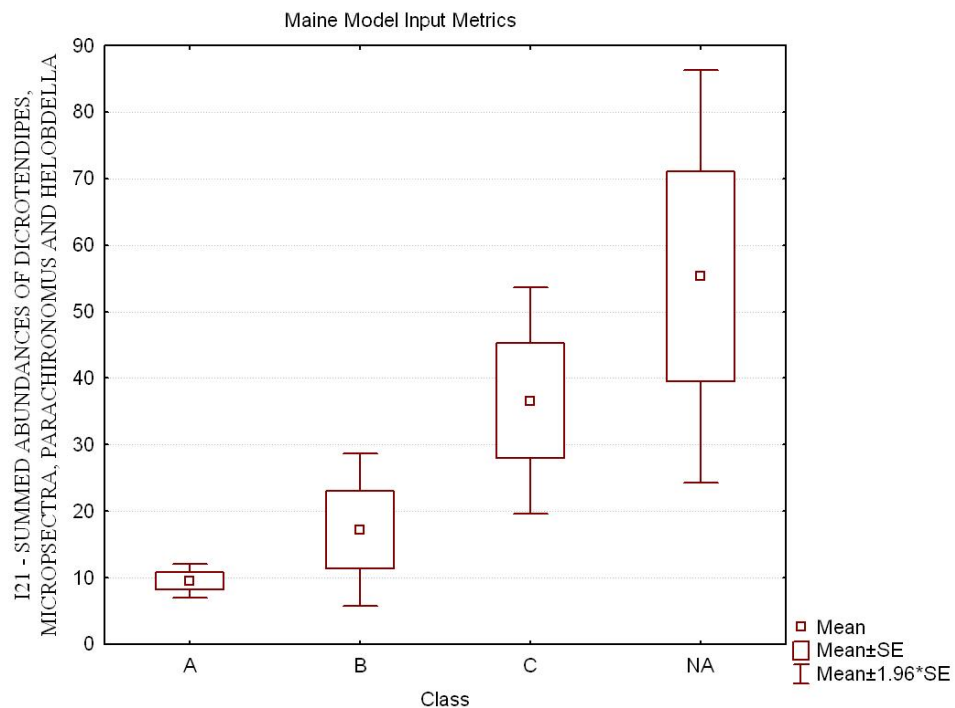
Figure C-19. Differences in total abundances of *Dicrotendipes*, *Micropsectra*, *Parachironomus*, and *Helobdella* by class.
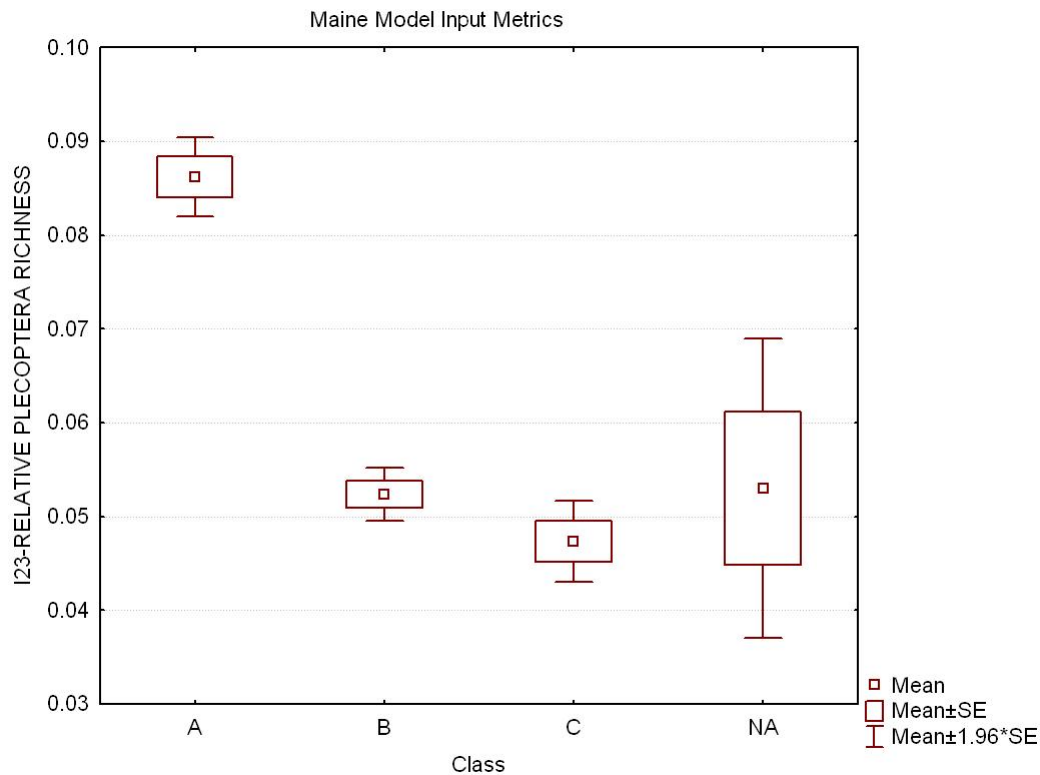
Figure C-20. Differences in relative Plecoptera richness by class.

C-18
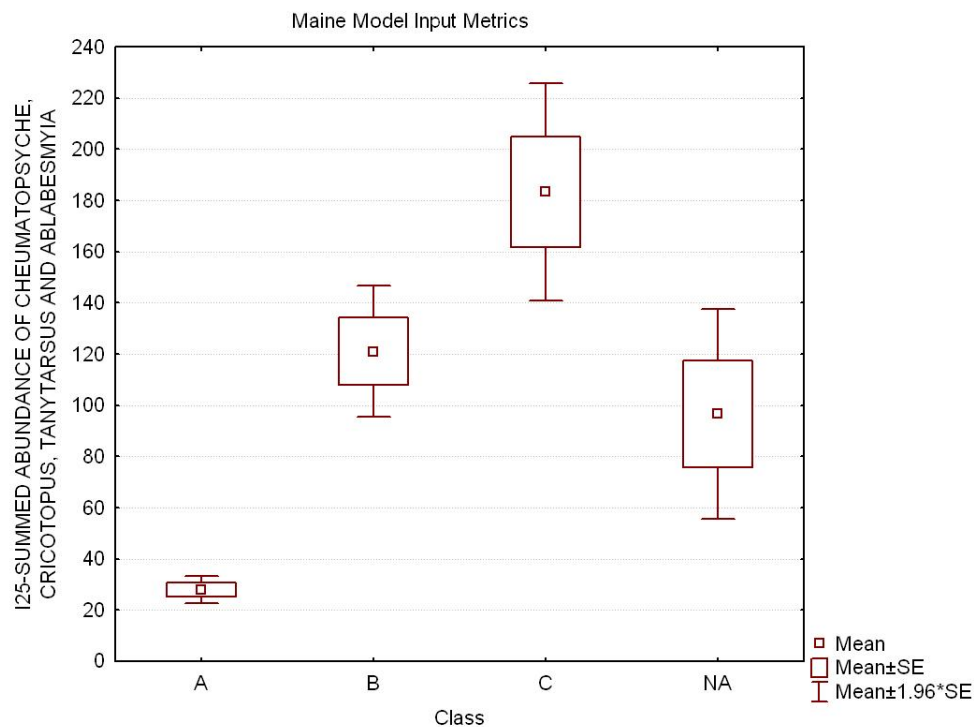
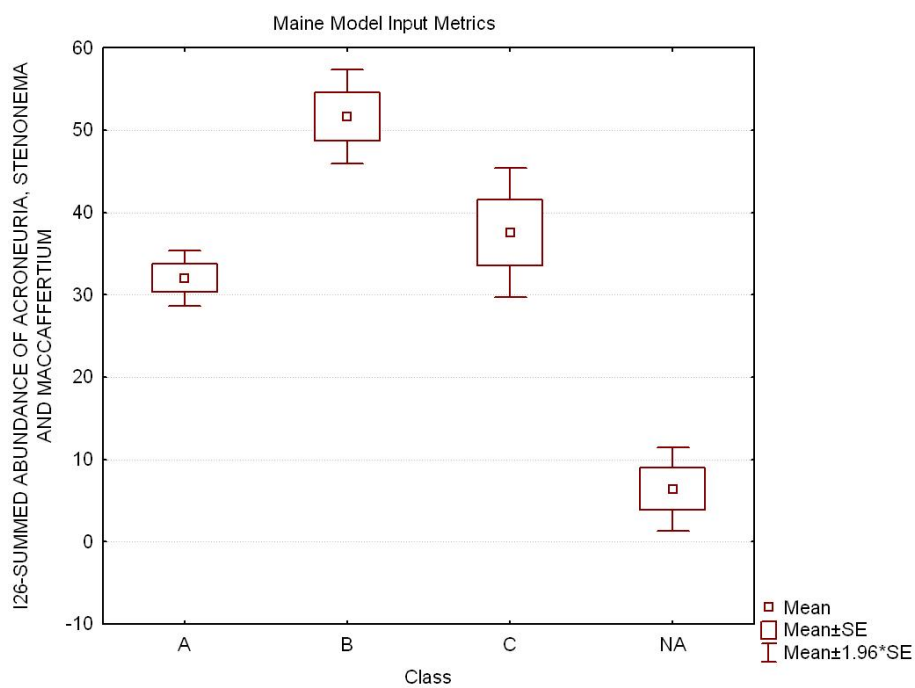**Figure C-21. Differences in total abundances of *Cheumatopsyche*, *Cricotopus*, *Tanytarsus,* and *Ablabesmyia* by class.**

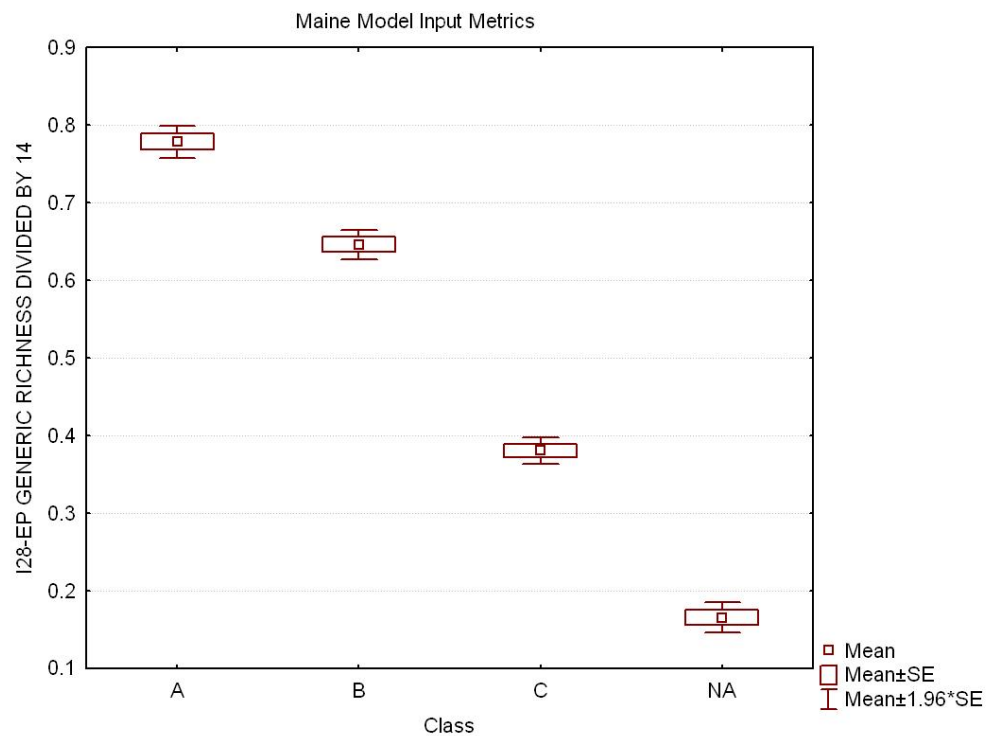**Figure C-22. Differences in total abundances of *Acroneuria*, *Stenonema*, and *Maccaffertium* by class.**
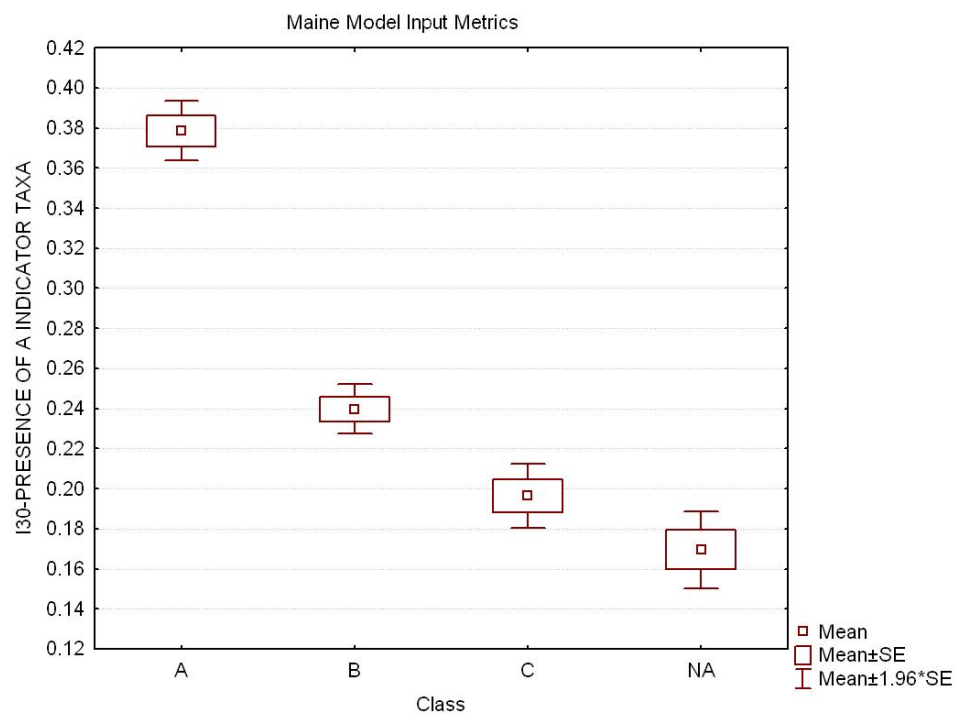
Figure C-23. Differences in EP richness by class.

Figure C-24. Differences in presence of indicator taxa by class.

C.3. DISTRIBUTION OF INDICATOR TAXA BY YEARS GROUPED AS CLIMATE SURROGATES

Figure C-25 shows indicator taxa grouped by driest-, normal-, and wettest-year samples, while Figure C-26 shows indicator taxa grouped by lowest-, normal-, and highest-flow year samples.
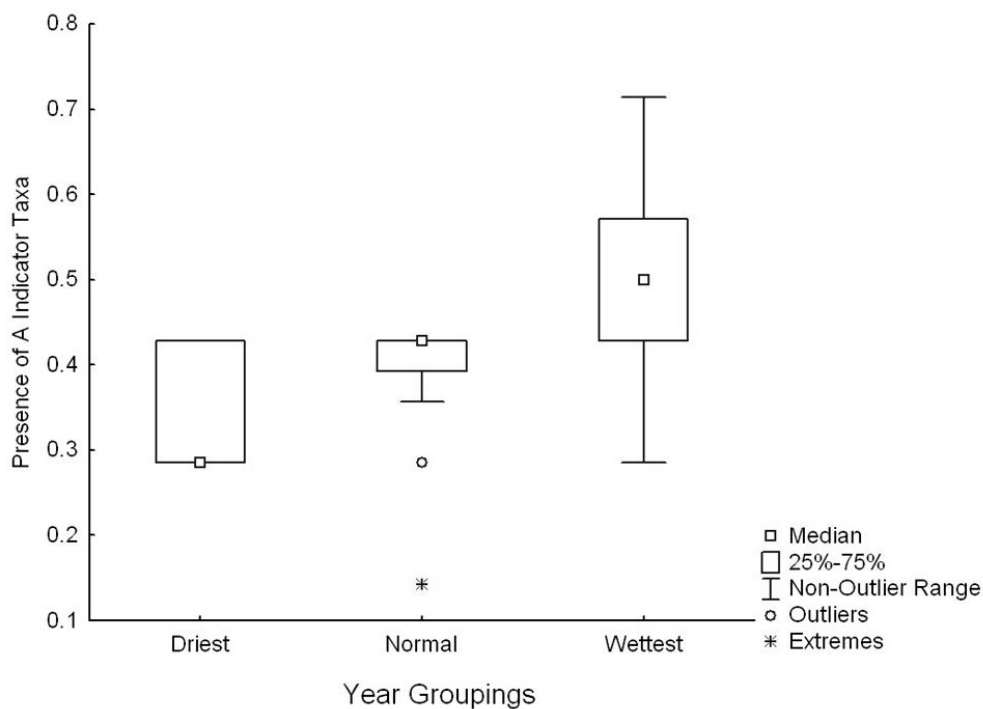

Figure C-25. Distributions of Class A indicator taxa metric values in driest-, normal-, and wettest-year samples at Maine site 56817 (Sheepscot). Year groupings are based on Parameter‑elevation Regressions on Independent Slopes Model (PRISM) mean annual precipitation from each site during time periods for which biological data were available. Data used in these analyses were limited to summer (July−September) rock-basket samples.
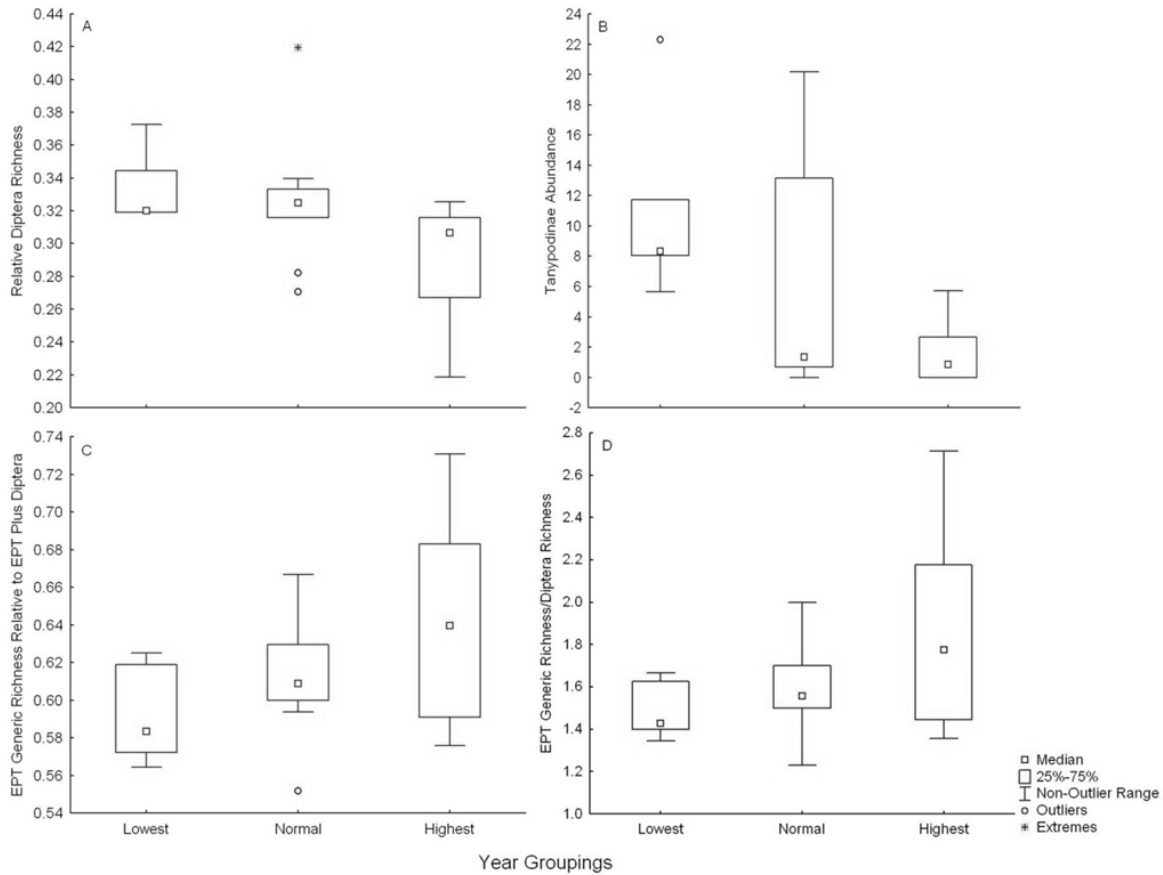
Figure C-26. Distributions of EPT and Dipteran-related metric values in lowest-, normal-, and highest-flow year samples at Maine site 56817 (Sheepscot). Plot (A) shows relative Diptera richness, (B) Tanypodinae abundance, (C) EPT generic richness relative to EPT plus Diptera, and (D) EPT generic richness/Diptera richness. Year groupings are based on IHA median monthly flows averaged across July−September. Data used in these analyses were limited to summer (July−September) rock-basket samples.